

SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Screening of genes to give tolerance against
environmental stress and the apprications

<130> 12-130

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<150> JP P1999-235910

<151> 1999-07-19

<150> JP P2000-85377

<151> 2000-03-24

<160> 66

<170> PatentIn Ver. 2.1

<210> 1

<211> 1018

<212> DNA

<213> Bruguiera sexangula

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<221> CDS

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Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys Val Val Gly Pro Ala
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aga tca aag agt gct act gta ccc acc caa aca gta ttg cct ttc aag 152
Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys
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Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys
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ggt tca agc ttt gac agc ttc tct gta ccc aaa aga tct ttt tct tgc 248
Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys Arg Ser Phe Ser Cys
55 60 65

aga agc caa gcc act cca tct gat gat gcc tca aga ccc acc aaa gtt 296
Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser Arg Pro Thr Lys Val
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caa gag ctg tgt gtg tat gag atg aac gag aga gat cgt gga agc cct 344

Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg Asp Arg Gly Ser Pro
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 Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn Ser Leu Gly Asp Leu
 105 110 115
 gtg cct ttc agt aac aaa gtt tac agc gga gac ctg cag aag cga att 440
 Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp Leu Gln Lys Arg Ile
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 Gly Val Thr Ala Glu Tyr Ala Ser
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<213> Bruguiera sexangula

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 35 40 45
 Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys
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 Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
 65 70 75 80
 Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
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Ser	Met	Lys	Val	Glu	Lys	Leu	Gly	Lys	Asp	Ser	Leu	Val	Asn	Cys	Ala	
140					145					150					155	
aag	aca	agc	atg	tcc	tca	aag	ttg	ata	gct	ggg	gac	agc	gac	ttc	ttt	593
Lys	Thr	Ser	Met	Ser	Ser	Lys	Leu	Ile	Ala	Gly	Asp	Ser	Asp	Phe	Phe	
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Ala	Asn	Leu	Val	Val	Asp	Ala	Val	Gln	Ala	Val	Lys	Met	Thr	Asn	Ala	
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Arg	Gly	Glu	Ile	Lys	Tyr	Pro	Ile	Lys	Ser	Ile	Asn	Ile	Leu	Lys	Ala	
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cat	gga	aaa	agt	gca	aga	gat	agc	tgc	ctt	ttg	aat	ggc	tat	gct	ctc	737
His	Gly	Lys	Ser	Ala	Arg	Asp	Ser	Cys	Leu	Leu	Asn	Gly	Tyr	Ala	Leu	
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Arg	Ile	Ala	Cys	Leu	Asp	Phe	Asn	Leu	Gln	Lys	Thr	Lys	Met	Gln	Leu	
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Gly	Val	Gln	Val	Leu	Val	Thr	Asp	Pro	Arg	Glu	Leu	Glu	Arg	Ile	Arg	
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Gln	Arg	Glu	Ala	Asp	Met	Thr	Lys	Glu	Arg	Ile	Glu	Lys	Leu	Leu	Lys	
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gct	gga	gca	aat	gtt	gtt	cta	acc	aca	aag	gga	att	gat	gac	atg	gca	977
Ala	Gly	Ala	Asn	Val	Val	Leu	Thr	Thr	Lys	Gly	Ile	Asp	Asp	Met	Ala	
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Leu	Lys	Tyr	Phe	Val	Glu	Ala	Gly	Ala	Ile	Ala	Val	Arg	Arg	Val	Arg	
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Lys	Glu	Asp	Met	Arg	His	Val	Ala	Lys	Ala	Thr	Gly	Ala	Thr	Leu	Val	
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Ser	Thr	Phe	Ala	Asp	Met	Glu	Gly	Glu	Glu	Thr	Phe	Asp	Ser	Ser	Leu	
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Leu Arg Gly Ala Asn Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu			
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His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val			
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Val Ala Gly Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu			
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Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala			
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gcc aaa gat gcc act gaa tta gct gca aaa ctc cgg gct tac cac cat			1505
Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His			
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aca gca caa aca aag gct gat aag aaa cat tta tca agc atg gga cta			1553
Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu			
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gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att			1601
Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile			
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gaa cct gca atg agc aaa ata aag ata att cag ttt gct act gaa gca			1649
Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala			
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gcc ata aca att ctt cga att gat gac atg atc aag ctt gtc aag gat			1697
Ala Ile Thr Ile Leu Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp			
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<212> PRT

<213> Bruguiera sexangula

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Asn	Lys	Ile	His	Pro	Thr	Ser	Ile	Ile	Ser	Gly	Tyr	Arg	Leu	Ala	Met
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Arg	Glu	Ala	Cys	Lys	Tyr	Val	Glu	Glu	Lys	Leu	Ser	Met	Lys	Val	Glu
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Ser	Lys	Leu	Ile	Ala	Gly	Asp	Ser	Asp	Phe	Phe	Ala	Asn	Leu	Val	Val
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Asp	Ala	Val	Gln	Ala	Val	Lys	Met	Thr	Asn	Ala	Arg	Gly	Glu	Ile	Lys
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Tyr	Pro	Ile	Lys	Ser	Ile	Asn	Ile	Leu	Lys	Ala	His	Gly	Lys	Ser	Ala
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Ala	Gln	Gly	Met	Pro	Met	Arg	Val	Ala	Pro	Ala	Arg	Ile	Ala	Cys	Leu
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Val	Thr	Asp	Pro	Arg	Glu	Leu	Glu	Arg	Ile	Arg	Gln	Arg	Glu	Ala	Asp	
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His	Val	Ala	Lys	Ala	Thr	Gly	Ala	Thr	Leu	Val	Ser	Thr	Phe	Ala	Asp	
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Met	Glu	Gly	Glu	Glu	Thr	Phe	Asp	Ser	Ser	Leu	Leu	Gly	Gln	Ala	Glu	
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Glu	Val	Val	Glu	Glu	Arg	Ile	Ala	Asp	Asp	Asp	Val	Ile	Met	Ile	Lys	
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Asp	Tyr	Met	Leu	Asp	Glu	Met	Glu	Arg	Ala	Leu	His	Asp	Ala	Leu	Cys	
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Ile	Val	Lys	Arg	Thr	Leu	Glu	Ser	Asn	Thr	Val	Val	Ala	Gly	Gly	Gly	
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Leu	Gly	Ser	Arg	Glu	Gln	Leu	Ala	Ile	Ala	Glu	Phe	Ala	Glu	Ser	Leu	
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Leu	Ile	Ile	Pro	Lys	Val	Leu	Ala	Val	Asn	Ala	Ala	Lys	Asp	Ala	Thr	
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Glu	Leu	Ala	Ala	Lys	Leu	Arg	Ala	Tyr	His	His	Thr	Ala	Gln	Thr	Lys	
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Thr	Ile	Arg	Asn	Asn	Leu	Glu	Ala	Gly	Val	Ile	Glu	Pro	Ala	Met	Ser	
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Lys	Ile	Lys	Ile	Ile	Gln	Phe	Ala	Thr	Glu	Ala	Ala	Ile	Thr	Ile	Leu	
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Cys Gly Ala Ser Cys Asn Cys Gly Asn Gly Cys Gly Gly Cys Lys Met
10 15 20 25

tac cca gac atg ggc ttc gcc gag aag acc act acc gag act ctg gtt 148
Tyr Pro Asp Met Gly Phe Ala Glu Lys Thr Thr Thr Glu Thr Leu Val
30 35 40

ctc ggc gtg ggg cct gag agg gcc cac ttt gag gga gcc gag atg ggc 196
Leu Gly Val Gly Pro Glu Arg Ala His Phe Glu Gly Ala Glu Met Gly
45 50 55

gtg ccg gcc gag aac gga ggc tgc aag tgc gga agt aac tgc acc tgc 244
Val Pro Ala Glu Asn Gly Gly Cys Lys Cys Gly Ser Asn Cys Thr Cys
60 65 70

gac ccc tgc act tgt aaa tgaggggaaa gtgacaggga aggtccgatc 292
Asp Pro Cys Thr Cys Lys
75

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cgtttcctcc atgcgcagat cttaggtttt aggatatctc tgtggtttct ccaagctatg 412
gattttcagt gtctagtttt cctgtattac aaggatagtt tataaccgta tatgcatggg 472
cggaatcctt ccaaccattt cgtttgtcta aatatatata tgtgtgtgtg tgtgtgtgtt 532
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Gly Ala Ala Ser Lys Thr Gly Lys Leu Thr Leu Lys Thr Thr Glu Met	
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gag acg gtg tac gat ttg ggg gcg aaa atg ata gag gca ttg ggg aag	144
Glu Thr Val Tyr Asp Leu Gly Ala Lys Met Ile Glu Ala Leu Gly Lys	
35 40 45	
gaa aag gtg cag agt ggg gat gtt att gca att gac aag gcg tcc ggc	192
Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly	
50 55 60	
aaa att aca aag ctt ggg cgt tca ttt tcg cgg tct agg gat tac gat	240
Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp	
65 70 75 80	
gcc atg gga cca cag gtg aag ttt gtt cag tgc cct gat ggg gag ctg	288
Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu	
85 90 95	
cag aag agg aaa gag gtc gtg cat tgt gtc tca ctg cac gag att gat	336
Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp	
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gtt atc aat agc aga aca cag ggg ttt ctt gct ctt ttc acc ggg gat	384
Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp	
115 120 125	

act ggt gaa atc cgt gcg gag gtg agg gaa caa att gac aca aag gtg	432
Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val	
130 135 140	
gct gaa tgg aga gag gaa ggg aaa gca gag att gtg cca ggt gtc ctc	480
Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu	
145 150 155 160	
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Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu	
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Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr	
180 185 190	
aac aga ggg atc acc aca atc aga ggc aca aat tac aaa tct cct cat	624
Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His	
195 200 205	
ggg att cca ata gat ctc ctt gat cga cta ctc att atc aca act caa	672
Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln	
210 215 220	
cct tac aca aag gat gaa att cgt aag att ctg gat atc aga tgt cag	720
Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln	
225 230 235 240	
gaa gaa gat gtg gag atg gct gaa gag gca aag gct ttg tta aca cat	768
Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His	
245 250 255	
att ggg gca gaa aca tcc ttg aga tat gcc atc cat ctc att act gct	816
Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala	
260 265 270	
gca gca ttg gca tgc cag aag cga aag gga aag ctt gtg gaa act gag	864
Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu	
275 280 285	
gac att agt cga gct tac aat ctg ttt ctt gat gta aag aga tct aca	912
Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr	
290 295 300	
cag tac cta ata gag tat cag aat cag tac atg ttt aat gag gca ccg	960
Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro	
305 310 315 320	
gta gga gaa ggg gac gaa gaa ggg gcc aat gcc atg ctt tct	1002
Val Gly Glu Gly Asp Glu Glu Gly Ala Asn Ala Met Leu Ser	
325 330	
tgaagggcca taagctatgg agtctttgtg aaacccttct ccctacttta ttcgcagcac	1062
gagccctgaa atgaagaaca atggtagact tggatcccac cttggccctt atgtatgtct	1122

tctggaattg aaaaaagagt ccaagaaatt tgaatttcac gaaattggag aactgaactg 1182
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 <213> Bruguiera sexangula

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 Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly
 50 55 60
 Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp
 65 70 75 80
 Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu
 85 90 95
 Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp
 100 105 110
 Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp
 115 120 125
 Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val
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 Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu
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 Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu
 165 170 175
 Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr
 180 185 190
 Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His
 195 200 205
 Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln
 210 215 220
 Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln
 225 230 235 240


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<400> 10
Met Gly His Ser Asn Val Trp Asn Ser His Pro Lys Asn Tyr Gly Pro
  1              5              10              15

Gly Ser Arg Ala Cys Arg Val Cys Gly Asn Pro His Gly Leu Ile Arg
      20              25              30

Lys Tyr Gly Leu Met Cys Cys Arg Gln Cys Phe Arg Ser Asn Ala Lys
      35              40              45

Glu Ile Gly Phe Ile Lys Tyr Arg
  50              55

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<220>  
<221> CDS  
<222> (34)..(1380)
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<400> 11																
tctctcttta	cagggttaaag	ctaagacttt	ata	atg	ggt	aag	gag	aag	att	cac						54
				Met	Gly	Lys	Glu	Lys	Ile	His						
				1				5								
att aac att gtg gtt att ggc cat gtc gac tcc gga aag tca acc aca																102
Ile Asn Ile Val Val Ile Gly His Val Asp Ser Gly Lys Ser Thr Thr																
	10				15				20							
act ggc cac ttg att tac aag ctt gga ggt atc gac aag cgt gtg att																150
Thr Gly His Leu Ile Tyr Lys Leu Gly Gly Ile Asp Lys Arg Val Ile																
	25				30				35							
gag agg ttt gag aag gaa gct gct gag atg aac aag agg tca ttc aag																198
Glu Arg Phe Glu Lys Glu Ala Ala Glu Met Asn Lys Arg Ser Phe Lys																
	40				45				50						55	
tat gcc tgg gtg ctt gac aag ctg aag gct gag cgt gag cgt ggt atc																246
Tyr Ala Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile																
			60					65					70			
acc att gat att gcc ttg tgg aag ttc gag aca acc aaa tat tac tgc																294
Thr Ile Asp Ile Ala Leu Trp Lys Phe Glu Thr Thr Lys Tyr Tyr Cys																
			75				80						85			
acg gtc att gat gct cct gga cat cgt gac ttt att aag aat atg atc																342
Thr Val Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile																
	90					95					100					

acc ggg act tcc caa gct gac tgt gct gtc ctc atc att gac tct acc	390
Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp Ser Thr	
105 110 115	
act ggt ggc ttt gag gct ggt atc tct aaa gat ggt cag acc cgc gag	438
Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr Arg Glu	
120 125 130 135	
cat gcc ctg ctt gcc ttc acc ctt ggt gtt aag caa atg att tgc tgc	486
His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile Cys Cys	
140 145 150	
tgc aac aag atg gat gct acc act tcc aag tat tct aag gca aga tat	534
Cys Asn Lys Met Asp Ala Thr Thr Ser Lys Tyr Ser Lys Ala Arg Tyr	
155 160 165	
gat gaa att gtt aag gaa gtg tca tcc tac ttg aag aag gtt ggt tac	582
Asp Glu Ile Val Lys Glu Val Ser Ser Tyr Leu Lys Lys Val Gly Tyr	
170 175 180	
aac cca gag aag att cct ttt gtc ccc ata tct gga ttt gag ggt gac	630
Asn Pro Glu Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu Gly Asp	
185 190 195	
aac atg att gag aga tcc acc aac ctt gac tgg tac aag ggc cca act	678
Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly Pro Thr	
200 205 210 215	
ctt ctt gag gcc ctg gac atg atc cag gag cca aag agg cca tca gat	726
Leu Leu Glu Ala Leu Asp Met Ile Gln Glu Pro Lys Arg Pro Ser Asp	
220 225 230	
aag ccc ctc cgt ctc cca ctt cag gat gtg tac aag att ggt ggt att	774
Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly Gly Ile	
235 240 245	
ggg aca gtc cca gtg ggt cgt gtt gaa act ggt gtc ctg aag cct gga	822
Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu Lys Pro Gly	
250 255 260	
atg gtt gtt act ttt ggt ccc tca gga ctg acc act gaa gtt aag tct	870
Met Val Val Thr Phe Gly Pro Ser Gly Leu Thr Thr Glu Val Lys Ser	
265 270 275	
gtg gag atg cac cat gaa gct ctc caa gag gct ctt ccc gga gac aac	918
Val Glu Met His His Glu Ala Leu Gln Glu Ala Leu Pro Gly Asp Asn	
280 285 290 295	
gtt ggc ttc aat gtt aag aat gtt tcc gtg aag gat ctt aag cgg ggt	966
Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Leu Lys Arg Gly	
300 305 310	
tat gtt gcc tca aac tcc aag gat gat cct gcc aag gag gca tct agc	1014
Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Glu Ala Ser Ser	
315 320 325	
ttc acc tcc caa gtt atc atc atg aac cac cct ggt cag att gga aat	1062

Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile Gly Asn
330 335 340
ggg tat gcc cct gtt ctg gat tgc cac acc tct cac att gct gtc aag 1110
Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala Val Lys
345 350 355
ttt tct gag atc ctc aca aag att gat agg cga tct ggc aag gag ctt 1158
Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys Glu Leu
360 365 370 375
gaa aag gag ccc aag ttc ttg aag aat ggt gat gct ggg ttc gtg aag 1206
Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Phe Val Lys
380 385 390
atg att ccg acc aag cct atg gtg gtg gaa act ttc tcc gag tat cct 1254
Met Ile Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu Tyr Pro
395 400 405
ccg ctt ggt aga ttt gcc gtc agg gac atg cgc cag act gtt gca gtg 1302
Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val Ala Val
410 415 420
gga gtc atc aag agt gtc gag aaa aag gaa cct tct gga gct aag gtg 1350
Gly Val Ile Lys Ser Val Glu Lys Lys Glu Pro Ser Gly Ala Lys Val
425 430 435
act aaa tct gct gcc aag aag ggt ggc aaa tgaaccgtgc aagtcagagt 1400
Thr Lys Ser Ala Ala Lys Lys Gly Gly Lys
440 445
tgatgtagat gaaggctatt ggaagaataa agactggggc ctggttagcg gtctaattat 1460
tgatgttca gcagttggtt tcgagaacta cagtttcaat tcagcgccat catcacggag 1520
ctgttggtcc cagaattggg ttcttgaccg tcggtggcat tggctggtgg tttgagtgc 1580
ttctttgtgt catgtttaga ctttatcgga tttgctatct cataaagcgg cttgggaatt 1640
ttaaaaaaaaa aaaaaaaaaa aaaa 1664

<210> 12

<211> 449

<212> PRT

<213> Bruguiera sexangula

<400> 12

Met Gly Lys Glu Lys Ile His Ile Asn Ile Val Val Ile Gly His Val
1 5 10 15
Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
20 25 30
Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
35 40 45

Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys	50	55	60	
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe	65	70	75	80
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg	85	90	95	
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala	100	105	110	
Val	Leu	Ile	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser	115	120	125	
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Leu	Ala	Phe	Thr	Leu	Gly	130	135	140	
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Ser	145	150	155	160
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Val	Lys	Glu	Val	Ser	Ser	165	170	175	
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Glu	Lys	Ile	Pro	Phe	Val	Pro	180	185	190	
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu	195	200	205	
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Met	Ile	Gln	210	215	220	
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp	225	230	235	240
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu	245	250	255	
Thr	Gly	Val	Leu	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Gly	Pro	Ser	Gly	260	265	270	
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ala	Leu	Gln	275	280	285	
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ser	290	295	300	
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp	305	310	315	320
Pro	Ala	Lys	Glu	Ala	Ser	Ser	Phe	Thr	Ser	Gln	Val	Ile	Ile	Met	Asn	325	330	335	
His	Pro	Gly	Gln	Ile	Gly	Asn	Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His	340	345	350	

Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp
 355 360 365
 Arg Arg Ser Gly Lys Glu Leu Glu Lys Glu Pro Lys Phe Leu Lys Asn
 370 375 380
 Gly Asp Ala Gly Phe Val Lys Met Ile Pro Thr Lys Pro Met Val Val
 385 390 395 400
 Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
 405 410 415
 Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Glu Lys Lys
 420 425 430
 Glu Pro Ser Gly Ala Lys Val Thr Lys Ser Ala Ala Lys Lys Gly Gly
 435 440 445
 Lys

<210> 13
 <211> 770
 <212> DNA
 <213> Bruguiera sexangula

<220>
 <221> CDS
 <222> (2) .. (769)

<400> 13
 c gat gat atg gac gag gcc aca ccc acc ttt gtt tgg ggc acc aat atc 49
 Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile
 1 5 10 15
 agc gtg cag gat gtc aag gcc gct att cag atg ttt ttg aag cac ttc 97
 Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe
 20 25 30
 agg gat agt aat cag agt caa agg aac gag att ttt gaa gaa ggg aag 145
 Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys
 35 40 45
 tac gtg aaa gcg ata cat aag gtt ctt gaa gtt gaa gga gag tcg ctt 193
 Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu
 50 55 60
 gat gtt gat gct cgt gat gtg ttt gat tat gat tct gat ttg tat gcc 241
 Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala
 65 70 75 80
 aag atg att cgg tac cca ctt gag gtt ttg gcc att ttc gac att gtt 289
 Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val
 85 90 95

ttg atg gat att gtg agt ttg atc aac cct ttg ttt gag aaa cat gta	337
Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val	
100 105 110	
caa gtc agg att ttc aat ctt aag acc tcg att aca atg aga aat ctc	385
Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu	
115 120 125	
aac cct tct gat atc gaa aag atg gtg tca ttg aag gga atg ata att	433
Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile	
130 135 140	
cgg tgt agt tcc ata ata ccg gag atc agg gaa gca gta ttt aga tgc	481
Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys	
145 150 155 160	
ctt gtt tgt ggc tac ttc tct gat ccc atc gtt gtg gat aga gga cgg	529
Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg	
165 170 175	
ata agt gaa cct aaa gca tgc ttg aaa gag gaa tgt ctt act aag aac	577
Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn	
180 185 190	
tcc atg aca cta gtt cac aat cgt tgc agg ttt gct gat aag cag att	625
Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile	
195 200 205	
gtg agg ctc cag gag aca cct gac gag atc cct gaa gga gga aca cca	673
Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro	
210 215 220	
cac acg gtg agc tta ttg atg cat gac aag ctg gta gat gct gga aag	721
His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys	
225 230 235 240	
cca ggt gac agg gtt gag gtc act gga att tat agg gct atg agt gtt a	770
Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val	
245 250 255	

<210> 14

<211> 256

<212> PRT

<213> Bruguiera sexangula

<400> 14

Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile
1 5 10 15

Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe
20 25 30

Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys
35 40 45

Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu

50					55					60					
Asp	Val	Asp	Ala	Arg	Asp	Val	Phe	Asp	Tyr	Asp	Ser	Asp	Leu	Tyr	Ala
65					70					75					80
Lys	Met	Ile	Arg	Tyr	Pro	Leu	Glu	Val	Leu	Ala	Ile	Phe	Asp	Ile	Val
				85					90					95	
Leu	Met	Asp	Ile	Val	Ser	Leu	Ile	Asn	Pro	Leu	Phe	Glu	Lys	His	Val
			100					105					110		
Gln	Val	Arg	Ile	Phe	Asn	Leu	Lys	Thr	Ser	Ile	Thr	Met	Arg	Asn	Leu
		115					120					125			
Asn	Pro	Ser	Asp	Ile	Glu	Lys	Met	Val	Ser	Leu	Lys	Gly	Met	Ile	Ile
		130					135					140			
Arg	Cys	Ser	Ser	Ile	Ile	Pro	Glu	Ile	Arg	Glu	Ala	Val	Phe	Arg	Cys
145						150					155				160
Leu	Val	Cys	Gly	Tyr	Phe	Ser	Asp	Pro	Ile	Val	Val	Asp	Arg	Gly	Arg
				165					170					175	
Ile	Ser	Glu	Pro	Lys	Ala	Cys	Leu	Lys	Glu	Glu	Cys	Leu	Thr	Lys	Asn
			180					185					190		
Ser	Met	Thr	Leu	Val	His	Asn	Arg	Cys	Arg	Phe	Ala	Asp	Lys	Gln	Ile
			195				200					205			
Val	Arg	Leu	Gln	Glu	Thr	Pro	Asp	Glu	Ile	Pro	Glu	Gly	Gly	Thr	Pro
		210					215					220			
His	Thr	Val	Ser	Leu	Leu	Met	His	Asp	Lys	Leu	Val	Asp	Ala	Gly	Lys
225						230					235				240
Pro	Gly	Asp	Arg	Val	Glu	Val	Thr	Gly	Ile	Tyr	Arg	Ala	Met	Ser	Val
				245					250					255	

<210> 15
 <211> 846
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (39) .. (530)

<400> 15
 caaattttct ttgctgaatc gaatctacaa aatacctg atg ggt cag gtt ctt gac 56
 Met Gly Gln Val Leu Asp
 1 5

aaa ttt caa cgt aag caa tgg aga caa aag caa atc cag aag ata aca 104
 Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys Gln Ile Gln Lys Ile Thr
 10 15 20

gat aag gta ttt gat cgt gtc aaa agt ccg acc gga aat ggc act ctt	152
Asp Lys Val Phe Asp Arg Val Lys Ser Pro Thr Gly Asn Gly Thr Leu	
25 30 35	
aca ttt gaa gag ctg tat ata gct acc ctg att gtc tac aat gat ata	200
Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu Ile Val Tyr Asn Asp Ile	
40 45 50	
aac aag tat ttg ccg ggg ccg cac ttt gat cct cca tcg aaa gac aaa	248
Asn Lys Tyr Leu Pro Gly Pro His Phe Asp Pro Pro Ser Lys Asp Lys	
55 60 65 70	
atc aga gcc ttg atg cag gaa tgc gat atg gat gtc gat gga gaa ctt	296
Ile Arg Ala Leu Met Gln Glu Cys Asp Met Asp Val Asp Gly Glu Leu	
75 80 85	
aac cgt gag gaa ttt gtg aag ttc atg cag aag gtg aca gcc gat aca	344
Asn Arg Glu Glu Phe Val Lys Phe Met Gln Lys Val Thr Ala Asp Thr	
90 95 100	
ttc tct acg gtc agc cag gga ctg att atc tct ctg att ctg gcg cca	392
Phe Ser Thr Val Ser Gln Gly Leu Ile Ile Ser Leu Ile Leu Ala Pro	
105 110 115	
aca gtt gca ttg gcg acg aag agg gca aca gaa ggt gtt cca ggt gtg	440
Thr Val Ala Leu Ala Thr Lys Arg Ala Thr Glu Gly Val Pro Gly Val	
120 125 130	
ggg aaa gtg gtg caa aag gtg cct act tca att tat gca tcc ctg gtg	488
Gly Lys Val Val Gln Lys Val Pro Thr Ser Ile Tyr Ala Ser Leu Val	
135 140 145 150	
acc ctt gtt gtc gtt gca atc caa act gct agc gag gga tgc	530
Thr Leu Val Val Val Ala Ile Gln Thr Ala Ser Glu Gly Cys	
155 160	
tgattagagg ctttagttac ttgttcatga tacagaagga acagtcttgg tcaatttatt	590
tctttttttaa taggacataa ggaagttgta tatctttctt ctttcttcta ccaggttttg	650
ggggaagttg gaaagaacat acaaattgatt tcaactgcgt attggctgat cctcccattt	710
attaaaaactt gtcgtgtcta gcatgagcga ttcaatattt gcaatatgca atatttgtaa	770
tgatgtctac attcagtgat tagtgtgatt gtgcagtttg ttgggaaaaa aaaaaaaaaa	830
aaaaaaaaa aaaaaa	846

<210> 16

<211> 164

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 16

Met Gly Gln Val Leu Asp Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys

1	5	10	15
Gln Ile Gln Lys Ile Thr Asp Lys Val Phe Asp Arg Val Lys Ser Pro	20	25	30
Thr Gly Asn Gly Thr Leu Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu	35	40	45
Ile Val Tyr Asn Asp Ile Asn Lys Tyr Leu Pro Gly Pro His Phe Asp	50	55	60
Pro Pro Ser Lys Asp Lys Ile Arg Ala Leu Met Gln Glu Cys Asp Met	65	70	75
Asp Val Asp Gly Glu Leu Asn Arg Glu Glu Phe Val Lys Phe Met Gln	85	90	95
Lys Val Thr Ala Asp Thr Phe Ser Thr Val Ser Gln Gly Leu Ile Ile	100	105	110
Ser Leu Ile Leu Ala Pro Thr Val Ala Leu Ala Thr Lys Arg Ala Thr	115	120	125
Glu Gly Val Pro-Gly Val Gly Lys Val Val Gln Lys Val Pro Thr Ser	130	135	140
Ile Tyr Ala Ser Leu Val Thr Leu Val Val Val Ala Ile Gln Thr Ala	145	150	155
			160
Ser Glu Gly Cys			

<210> 17
 <211> 872
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (183)..(569)

<400> 17
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 agtaagctct gtccttttgc tctctgttga atgtactatc ttctgtgaac caaaggccaa 120
 agattaacta ttggagattt ctctactcga aatttggttt taggtgttga ccctgttgag 180
 ct atg gcg aac aag ccc caa att cca acg aag aat tcg gcc ctc att 227
 Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile
 1 5 10 15
 gct att atc gcg gat gag gat act gta act gga ttt ttg ctg gct gga 275
 Ala Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly
 20 25 30

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gtt ggt aat gtt gat cta cga aga cag aca aat tac att att gtg gac 323
Val Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp
      35              40              45

aat aaa aca acg atg aag caa atc gaa gat gca ttc aag gag ttc aca 371
Asn Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr
      50              55              60

gca aga gag gac att gcg gtt gta cta atc agc caa tat gtt gca aat 419
Ala Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn
      65              70              75

atg ata aga gta ttg gtt gat agc tac aac aaa cca atc ccg gca att 467
Met Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile
      80              85              90              95

ttg gag att cct tca aag gac cat cct tat gat cct aac cat gat tca 515
Leu Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser
      100              105              110

gtc ctt tca agg gtt aaa tac ctg ttc tct tct gaa tcg gca tca agc 563
Val Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser
      115              120              125

aga ttt tagccatg ctttgtaaag ttccctgctc ctgaatgttt ggtgattatg 619
Arg Phe

agtttaaact agaaccagtc acattctgac ttggatattt gaggcactgt ttgttttatg 679

ttcttaaaat aaggagtgtg attacgactc catgaatcgg gatatgactc catgaatcgc 739

atgtatttct ttccatctca tttgaaagag tcgagcagcc atatcattta gtttcttcct 799

cttgccaatg agcttggaag aaatgttttg gctataaaag atttcaactc ttggtacaaa 859

aaaaaaaaaa aaa 872

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<210> 18
<211> 129
<212> PRT
<213> Mesembryanthemum crystallinum

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<400> 18
Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile Ala
  1              5              10              15

Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly Val
      20              25              30

Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp Asn
      35              40              45

Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr Ala
      50              55              60

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Arg	Glu	Asp	Ile	Ala	Val	Val	Leu	Ile	Ser	Gln	Tyr	Val	Ala	Asn	Met	
65					70					75					80	
Ile	Arg	Val	Leu	Val	Asp	Ser	Tyr	Asn	Lys	Pro	Ile	Pro	Ala	Ile	Leu	
				85					90					95		
Glu	Ile	Pro	Ser	Lys	Asp	His	Pro	Tyr	Asp	Pro	Asn	His	Asp	Ser	Val	
			100					105					110			
Leu	Ser	Arg	Val	Lys	Tyr	Leu	Phe	Ser	Ser	Glu	Ser	Ala	Ser	Ser	Arg	
		115					120					125				

Phe

<210> 19
 <211> 647
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (64) .. (426)

<400> 19
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aca	atg	gcg	tac	gcg	atg	aag	cca	acg	aag	ccc	ggg	atg	gag	gaa	tcc	108
Met	Ala	Tyr	Ala	Met	Lys	Pro	Thr	Lys	Pro	Gly	Met	Glu	Glu	Glu	Ser	
1				5					10					15		
cag	gag	cag	att	cac	aag	atc	agg	atc	act	ctt	tct	tct	aag	aac	gtc	156
Gln	Glu	Gln	Ile	His	Lys	Ile	Arg	Ile	Thr	Leu	Ser	Ser	Lys	Asn	Val	
				20				25						30		
aag	aac	ctt	gag	aaa	gtg	tgt	gct	gat	ctt	gta	cgc	ggg	gca	aag	gac	204
Lys	Asn	Leu	Glu	Lys	Val	Cys	Ala	Asp	Leu	Val	Arg	Gly	Ala	Lys	Asp	
			35				40					45				
aag	cgc	ctc	agg	gtt	aag	gga	cca	gtg	agg	atg	ccc	acc	aag	gtt	ctg	252
Lys	Arg	Leu	Arg	Val	Lys	Gly	Pro	Val	Arg	Met	Pro	Thr	Lys	Val	Leu	
			50				55				60					
aag	atc	aca	aca	agg	aag	tct	ccc	tgt	ggg	gaa	gga	acc	aac	acc	ttt	300
Lys	Ile	Thr	Thr	Arg	Lys	Ser	Pro	Cys	Gly	Glu	Gly	Thr	Asn	Thr	Phe	
	65					70					75					
gac	aga	ttt	gag	ttg	cgt	gtt	cac	aag	aga	gtc	att	gac	ctc	ttc	agc	348
Asp	Arg	Phe	Glu	Leu	Arg	Val	His	Lys	Arg	Val	Ile	Asp	Leu	Phe	Ser	
	80				85				90						95	
tcc	cca	gac	gtg	gtc	aag	cag	atc	acc	tcc	atc	acc	att	gaa	cct	ggg	396
Ser	Pro	Asp	Val	Val	Lys	Gln	Ile	Thr	Ser	Ile	Thr	Ile	Glu	Pro	Gly	
				100					105					110		

gtt gag gtt gag gtt aca ata gct gac tct tagacatgcc tgttgaagtt 446
 Val Glu Val Glu Val Thr Ile Ala Asp Ser
 115 120

gtcgtcgttg tagggctggt gtagctgtct catatagtgg tgctatctca ctaagaattt 506
 tgaagatact aaattgtttg tttgaaagag atgttttctt tagctgtaat gttatgtttt 566
 tgaagggtgtt ggaacatgca ttatttgta atgctttatc aatagaactt ccaatttgaa 626
 tgcaaaaaaaaa a 647

<210> 20
 <211> 121
 <212> PRT
 <213> Mesembryanthemum crystallinum

<400> 20
 Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser Gln
 1 5 10 15
 Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys
 20 25 30
 Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp Lys
 35 40 45
 Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu Lys
 50 55 60
 Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe Asp
 65 70 75 80
 Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser Ser
 85 90 95
 Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly Val
 100 105 110
 Glu Val Glu Val Thr Ile Ala Asp Ser
 115 120

<210> 21
 <211> 686
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (62) .. (493)

<400> 21
 acaccattca caaacacat taaaaaaaa cactacttct ttctttctta gccacttgaa 60


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a atg gcc tac tca aag gct gta ctc ctt gcc ctt atc ttt gct gtg act 109
Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr
  1           5           10          15

ctt gtc att gcc tct cag gtc tca gct cgt gaa ctt gct gag gag aca 157
Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr
      20           25           30

caa tct gtg gag gag tct aag gga tac ggt ggt ggg cac gga ggt cac 205
Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His
      35           40           45

tat ggt ggt ggt cac tat ggt ggt gga cac aga cac ggt ggc cat gga 253
Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly
      50           55           60

cac tac gca act gag gaa gca gag aac aag aat gaa gcc gta gaa cct 301
His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro
      65           70           75           80

caa ggc ggc tat ggt cac gga cac gga gga ggc tac gga cac ggt ggt 349
Gln Gly Gly Tyr Gly His Gly His Gly Gly Gly Tyr Gly His Gly Gly
      85           90           95

ggc tac gga cac ggt gga ggc tac gga cac gga ggt ggc tac ggg cac 397
Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His
      100          105          110

ggc ggt ggc tac gga cat gga ggt ggt tat gga cac ggt gga cac ggt 445
Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly
      115          120          125

gga cat ggt ggt cat ggt cac tac gcc aag act acc gag gaa caa aat 493
Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn
      130          135          140

taagttatgg gttactaaaa cttaaattgt acgttggtcaa ataaaaatgta ctttatgatt 553

ttacatgagt atgcatgtaa ttcatacataa gcttcaagga ctatcttgta ctctatgtta 613

tataacctata tgaaatggaa gcgtgacttt tattactgta aaaaaaaaaa aaaaaaaaaa 673

aaaaaaaaaa aaa 686

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<210> 22

<211> 144

<212> PRT

<213> Sueada japonica

<400> 22

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Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr
  1           5           10          15

Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr
      20           25           30

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35	40	45
Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly		
50	55	60
His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro		
65	70	75 80
Gln Gly Gly Tyr Gly His Gly His Gly Gly Gly Tyr Gly His Gly Gly		
85	90	95
Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His		
100	105	110
Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly		
115	120	125
Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn		
130	135	140

<210> 23
 <211> 683
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (48) .. (362)

<400> 23	
gttaagatat tatattgcaa ctttacaaag catttctgca actaaat atg gcc ttt	56
	Met Ala Phe
	1
tcc aaa cct cta att gct tct cta ctt ctt tct ctc ttt gtt ctt cag	104
Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe Val Leu Gln	
5	10 15
ttt gtt cat gca gtt gaa cct att tca tcc tcc aat caa gtg ggt agc	152
Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln Val Gly Ser	
20	25 30 35
aac act gga ggt acc tca gag agt aaa gtg gat tgt ggg gcg gca tgt	200
Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly Ala Ala Cys	
40	45 50
acg gtg agg tgc agc gcc tcg aag agg cca aac cta tgc aac agg tca	248
Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys Asn Arg Ser	
55	60 65
tgt ggc agt tgt tgc aag acg tgc aac tgc gtg cca cca ggc act tcc	296
Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro Gly Thr Ser	
70	75 80
ggc aac tac gaa gcc tgc cct tgt tac gcc aac ttg acc acc cac ggc	344

Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His

,P□^,X,P

Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr Thr His Gly
85 90 95

aat cga cac aag tgc cct taattaacaa gaattgttta gttgtttatt 392
Asn Arg His Lys Cys Pro
100 105

acatccgtac catgtaacgt actcctatatt acactactag agtactagta ataaacattt 452
ttaggcacgg tccagttggt catgtagcta gtggtatatt gagtcataaa tgagtgattg 512
aaaatgagat atgataaaag tgtattatct acattgtagt actgttttgt atcatagtgt 572
agtgatgttt atttttcgta cttttaattt gttactttgt attccctttc attctatcta 632
tttacaatcc ttttgaagt ttatgtgaaa aaaaaaaaaa a 683

<210> 24
<211> 105
<212> PRT
<213> Salsola komarovii

<400> 24
Met Ala Phe Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe
1 5 10 15
Val Leu Gln Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln
20 25 30
Val Gly Ser Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly
35 40 45
Ala Ala Cys Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys
50 55 60
Asn Arg Ser Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro
65 70 75 80
Gly Thr Ser Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr
85 90 95
Thr His Gly Asn Arg His Lys Cys Pro
100 105

<210> 25
<211> 803
<212> DNA
<213> Salsola komarovii

<220>
<221> CDS
<222> (51) .. (593)

<400> 25

cgcagacgct tcagctcttt ctctctcttt ctctctcttc accgtgaaag atg ggg	56
Met Gly	
1	
ttg tca ttt acc aaa ttg ttt agc cgg ttg ttc gct aag aag gaa atg	104
Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys Glu Met	
5 10 15	
cgt atc ctt atg gtc ggt ctc gat gcc gct ggt aaa acc acc att ctc	152
Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu	
20 25 30	
tat aaa ctc aag ctg gga gag att gtc acc acc att cct acc att gga	200
Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly	
35 40 45 50	
ttt aat gtg gag act gta gaa tac aag aac atc agc ttc act gtg tgg	248
Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp	
55 60 65	
gat gtc ggg ggt caa gac aag att cgt cca ttg tgg aga cat tac ttc	296
Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe	
70 75 80	
caa aac acc caa ggt ctc atc ttt gtg gtt gac agt aat gat cgt gac	344
Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg Asp	
85 90 95	
cgt gtc gtt gag gca aga gat gaa ctg cat agg atg tta aat gag gat	392
Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu Asp	
100 105 110	
gaa tta cga gat gca gtg ttg ttg gtg ttt gca aac aag caa gat ctt	440
Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp Leu	
115 120 125 130	
ccc aat gca atg aat gct gct gag atc act gat aag ctt ggt ctc cat	488
Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu His	
135 140 145	
tct cta cgt caa cgc cat tgg tac ata caa agc aca tgt gcc acc tct	536
Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala Thr Ser	
150 155 160	
gga gaa ggg ctt tac gag ggt ctg gac tgg ctc tca aac aat atc gct	584
Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile Ala	
165 170 175	
agc aag gct taaaagtaac agaacgagta aggttagctt tctcagagaa	633
Ser Lys Ala	
180	
gaagctggag tataggctga ggactatcgt tactgctagt gttacccttt ttatttttgc	693
catttatatg ttcacatttt tggttcctat cggacaagaa ttatttttctg cgtttatgtt	753
gacttggttat aataccatac ttttttagttg aaaaaaaaaa aaaaaaaaaa	803

<210> 26
<211> 181
<212> PRT
<213> Salsola komarovii

<400> 26
Met Gly Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys
1 5 10 15
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr
20 25 30
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr
35 40 45
Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr
50 55 60
Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His
65 70 75 80
Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp
85 90 95
Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn
100 105 110
Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln
115 120 125
Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly
130 135 140
Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala
145 150 155 160
Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn
165 170 175
Ile Ala Ser Lys Ala
180

<210> 27
<211> 680
<212> DNA
<213> Avicennia marina

<220>
<221> CDS
<222> (161)..(454)

<400> 27
ctaaaagcca aaggcaagat aagaaacagg ttccttttagc tatcttcctc gtctcgctgc 60

Asp Pro Asp Thr Gly Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala
 65 70 75 80

Leu Asp Pro Val Glu Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser
 85 90 95

Arg Gln

<210> 29

<211> 490

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (20) .. (349)

<400> 29

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tcggctgggc aaagaaggg atg gcg att cca tcg gaa att cgg gac ttt att 52
                Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile
                  1             5             10

gct agc cgc aac aga tct ttg gtg atc gca tct cca aag gaa gat gag 100
Ala Ser Arg Asn Arg Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu
              15             20             25

aaa att ctc cgc tca agg cag tgc acc gaa gaa ggg gcg cgt gca gga 148
Lys Ile Leu Arg Ser Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly
              30             35             40

gcc aaa gct gct gca gtt gct tgc gtt gcc agc gcc att ccc act ctg 196
Ala Lys Ala Ala Ala Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu
              45             50             55

gta gct gtt cga acg att ccg tgg gca aag gca aac ctc aac tat aca 244
Val Ala Val Arg Thr Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr
              60             65             70             75

gcc cag gca ctc att ata tct tct gca tcc ata gcg gca tac ttt atc 292
Ala Gln Ala Leu Ile Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile
              80             85             90

gct gct gac aaa acc atc tta gag tgc gca cgg aaa aat gca gag tac 340
Ala Ala Asp Lys Thr Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr
              95             100             105

aaa tcg gct taagatgatg tgtaagacaa tgtgctcagc ttgcaatgct 389
Lys Ser Ala
              110

tgccatgact tgtgtttatg tgtatttcaa gtttctgaaa ctagcatttt gattttgtgt 449

tccaatgcaa tgagcattat ggaaaaaaaa aaaaaaaaaa a 490

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<210> 30
 <211> 110
 <212> PRT
 <213> Avicennia marina

<400> 30
 Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile Ala Ser Arg Asn Arg
 1 5 10 15
 Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu Lys Ile Leu Arg Ser
 20 25 30
 Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly Ala Lys Ala Ala Ala
 35 40 45
 Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu Val Ala Val Arg Thr
 50 55 60
 Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr Ala Gln Ala Leu Ile
 65 70 75 80
 Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile Ala Ala Asp Lys Thr
 85 90 95
 Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr Lys Ser Ala
 100 105 110

<210> 31
 <211> 592
 <212> DNA
 <213> Avicennia marina

<220>
 <221> CDS
 <222> (75)..(320)

<400> 31
 gcagtcctcag ccttcctgct ctctggtgc cttcaaattt gtgaatttct cgagtgctaa 60
 aagattcagc caag atg cag aac gaa gag ggg caa aac atg gat ctc tac 110
 Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr
 1 5 10
 atc ccc agg aaa tgc tct gcc acg aac agg ctg atc acc tcc aag gat 158
 Ile Pro Arg Lys Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp
 15 20 25
 cat gct tct gtc cag atc aat gtt ggg cac ttg gat gag aat ggc cga 206
 His Ala Ser Val Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg
 30 35 40
 tac act ggc caa tac tct acc ttt gct ctt tgt gga ttc atc cgt gct 254
 Tyr Thr Gly Gln Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala

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45          50          55          60
cag ggt gat gct gac agt gct ctt gat agg ctc tgg cag aaa aag aaa 302
Gln Gly Asp Ala Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys
          65          70          75

gtc gaa acc agg cag cag tgatcctgct caattcagca gtgaaagttt 350
Val Glu Thr Arg Gln Gln
          80

tttggggtttt gttctgtggt gtgttattta tgcttttcca gaatcaattt ctgtactgga 410
ttgagtatta aaaatgtgga gctaaagggtt gggagacctg atgcctttgt tactcgagta 470
atcacaagta gatactgggc ttgtaatagc gtgataattg tgccttgctc ttgcctcatt 530
gactacgaat cagttatgtg attagacaat gttaatctcc aaaaaaaaaa aaaaaaaaaa 590
aa 592

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<210> 32
<211> 82
<212> PRT
<213> Avicennia marina

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<400> 32
Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr Ile Pro Arg Lys
 1          5          10          15
Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val
          20          25          30
Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg Tyr Thr Gly Gln
          35          40          45
Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala Gln Gly Asp Ala
          50          55          60
Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Thr Arg
          65          70          75          80
Gln Gln

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<210> 33
<211> 1806
<212> DNA
<213> Avicennia marina

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<220>
<221> CDS
<222> (362) .. (1552)

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<400> 33

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tgtgaaggta aagtctacag catatttcgc gccgctcggt tgattacgtg ttgcttttat 60
 ttgggaattt gatagcgctg agtagccgat gccgctggag ggtattgttg attttaggaa 120
 tacgggtttg tttgattcgc agttttactg tctctagggt tgggccctga ggcttctggg 180
 atttgggatt taatcgctga tcgaacagtt tcctggagaa aatactccta gtgcgcatat 240
 atctgatttg ctgacgagaa attgatacac ggttatgcga ttgagttttg tttgcgccaa 300
 agatactccg agtgctcgct agatgtggat aatccggagg gctgtttcga tgagatgagg 360
 g atg tta tca ggg tta atg aac ttc ctg tgg gcc tgt ttt cgg cca agg 409
 Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg
 1 5 10 15
 gcg gat cga agt gtt cac acg ggt tca gat gca ggc ggt cgt cag gat 457
 Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp
 20 25 30
 ggg ctt tta tgg tat aag gac ttg ggg caa cat atc aat gga gag ttt 505
 Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
 35 40 45
 tca atg gct gta gtt caa gca aat aac tta cta gag gat cag agt caa 553
 Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln
 50 55 60
 ctt gaa tct ggt tgc ctg agc ttg agt gat tca gga caa tat ggc act 601
 Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr
 65 70 75 80
 ttt gtg ggg att tat gat gga cat gga ggt cct gag acc tct cgg ttt 649
 Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe
 85 90 95
 atc aat gac cat ctc ttc caa cat ata aag aga ttc aca gct gag cat 697
 Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His
 100 105 110
 caa tca atg tca gct gag gtc att cac aag gcc att caa gcg act gaa 745
 Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu
 115 120 125
 gaa ggt ttt ttc tcg gtt gtt agc aga caa tgg tcc atg caa cca cag 793
 Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln
 130 135 140
 att gca gca gtt ggc tct tgc tgc ctt gtt ggt gtc atc tgt agt ggc 841
 Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly
 145 150 155 160
 act ctt tat gtt tcc aac ctt ggt gat tcc cgt gct gtt ctt ggg acg 889
 Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr
 165 170 175
 ctt tcc aag gct aca ggg gaa gta cag gct act caa ctc tca aca gag 937

Leu	Ser	Lys	Ala	Thr	Gly	Glu	Val	Gln	Ala	Thr	Gln	Leu	Ser	Thr	Glu	
			180					185					190			
cat	aat	gca	agt	ttt	gag	tct	gtg	aga	cgg	gaa	ctg	cag	tct	ctg	cac	985
His	Asn	Ala	Ser	Phe	Glu	Ser	Val	Arg	Arg	Glu	Leu	Gln	Ser	Leu	His	
		195					200					205				
cca	gat	gac	tca	cag	att	gtg	gtt	cta	aag	cat	aat	gta	tgg	cga	gtg	1033
Pro	Asp	Asp	Ser	Gln	Ile	Val	Val	Leu	Lys	His	Asn	Val	Trp	Arg	Val	
		210				215					220					
aag	ggg	ctt	ata	cag	atc	tca	aga	tca	att	gga	gat	gtg	tat	ttg	aaa	1081
Lys	Gly	Leu	Ile	Gln	Ile	Ser	Arg	Ser	Ile	Gly	Asp	Val	Tyr	Leu	Lys	
225					230					235					240	
aag	gct	gaa	ttc	aac	agg	gag	cct	cta	tat	cag	aaa	ttt	cga	ctt	cgt	1129
Lys	Ala	Glu	Phe	Asn	Arg	Glu	Pro	Leu	Tyr	Gln	Lys	Phe	Arg	Leu	Arg	
				245					250					255		
gaa	gct	ttc	aaa	aga	cca	att	ttg	agc	tca	gaa	cca	gaa	act	act	gtg	1177
Glu	Ala	Phe	Lys	Arg	Pro	Ile	Leu	Ser	Ser	Glu	Pro	Glu	Thr	Thr	Val	
			260					265					270			
cac	cag	ctg	ctg	cct	cat	gat	caa	ttc	att	atc	ttc	gca	tca	gat	ggc	1225
His	Gln	Leu	Leu	Pro	His	Asp	Gln	Phe	Ile	Ile	Phe	Ala	Ser	Asp	Gly	
			275				280					285				
ctt	tgg	gag	cac	ctt	tcc	aac	caa	gaa	gca	gtt	gat	ctt	gtt	cag	aaa	1273
Leu	Trp	Glu	His	Leu	Ser	Asn	Gln	Glu	Ala	Val	Asp	Leu	Val	Gln	Lys	
						295					300					
cat	cca	cac	aat	ggg	att	gct	aga	aga	tta	gta	aaa	gca	gct	ttg	caa	1321
His	Pro	His	Asn	Gly	Ile	Ala	Arg	Arg	Leu	Val	Lys	Ala	Ala	Leu	Gln	
305					310				315						320	
gag	gca	gca	aag	aaa	agg	gaa	atg	agg	tac	tcg	gat	ttg	aag	aaa	att	1369
Glu	Ala	Ala	Lys	Lys	Arg	Glu	Met	Arg	Tyr	Ser	Asp	Leu	Lys	Lys	Ile	
				325					330					335		
gac	cgt	ggg	gtt	cgc	cgt	cat	ttc	cat	gat	gac	atc	act	gtt	gtg	gtg	1417
Asp	Arg	Gly	Val	Arg	Arg	His	Phe	His	Asp	Asp	Ile	Thr	Val	Val	Val	
			340					345					350			
gtg	ttt	ctt	gac	tca	cac	ctt	gtg	agc	cgg	gct	agc	tca	gtc	cgg	ggc	1465
Val	Phe	Leu	Asp	Ser	His	Leu	Val	Ser	Arg	Ala	Ser	Ser	Val	Arg	Gly	
		355					360					365				
cca	aac	atc	tcc	gtg	aaa	ggg	ggc	ggc	atc	agt	ctg	cct	ccc	aat	gct	1513
Pro	Asn	Ile	Ser	Val	Lys	Gly	Gly	Gly	Ile	Ser	Leu	Pro	Pro	Asn	Ala	
						375					380					
ctt	gca	cct	tgt	gcc	aca	cca	acg	gag	cca	gtc	cca	aat	tgatactgct			1562
Leu	Ala	Pro	Cys	Ala	Thr	Pro	Thr	Glu	Pro	Val	Pro	Pro	As			

gcttcttaac ggataacagc ggcccttgaa ttctttaatc cataactgtaa cttttaaccg 1682
gagactatta cttggcatag tttcaatgcc caagggatac atagactggg acaagccatc 1742
ttggcgggtga caatcatcat agttaagttt tctgggcata tctttcaaaa aaaaaaaaaa 1802
aaaa 1806

<210> 34
<211> 397
<212> PRT
<213> Avicennia marina

<400> 34
Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg
1 5 10 15
Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp
20 25 30
Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
35 40 45
Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln
50 55 60
Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr
65 70 75 80
Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe
85 90 95
Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His
100 105 110
Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu
115 120 125
Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln
130 135 140
Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly
145 150 155 160
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr
165 170 175
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu
180 185 190
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His
195 200 205
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val
210 215 220

Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys
 225 230 235 240
 Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg
 245 250 255
 Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val
 260 265 270
 His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly
 275 280 285
 Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys
 290 295 300
 His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln
 305 310 315 320
 Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile
 325 330 335
 Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val
 340 345 350
 Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly
 355 360 365
 Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala
 370 375 380
 Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn
 385 390 395

<210> 35
 <211> 743
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (1)..(420)

<400> 35
 cct gag cta gca cct aaa gat ggg gat ttc cgt ttc aat atc tct gag 48
 Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu
 1 5 10 15
 ctt gaa gct atg cta cca gct gga act gta gat cat gct gtt gaa agg 96
 Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg
 20 25 30
 att tat caa gag atg ccg cgg tgg gaa gag act gtt tta ggt tcc agg 144
 Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg
 35 40 45

agc aga tat gag cat gtc att cag gca ctt gca gat aaa tac cct tca 192
 Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser
 50 55 60

gaa aat ttg ttg cta gtt acg cat ggt gaa ggt gtt ggg act tca gtt 240
 Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val
 65 70 75 80

gca acg ttt ttg aaa ggc gct gtt gtt tat gaa gta aag tat tgt gct 288
 Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala
 85 90 95

tat tca caa gca aca aga cgc atc agc tat gga gaa ggc gag tca ttt 336
 Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe
 100 105 110

act gct ggt acc ttt cag ttg gtc act gcc tca gac caa acc ggt att 384
 Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile
 115 120 125

ggt tac tac aca tct agc agc ttg tct gat ggt gta tgacttatcg 430
 Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val
 130 135 140

gaactcccgga gtttctgcat tctgaaaggt gctttttgat ttccgaataa ttcttcaaatt 490
 ccacatgtca gaagatccat tcttttaggtc agatgtctat ctactgctcc cagccttgag 550
 ctgctcatgg gtattggtgc ccttctatatt ttaggttagag tcttttgagta agccttgcca 610
 catcaaggcc tcagattatt gaatgtacaa cagaataggt tgtagcttca ttggctagta 670
 cagtgacctc tttcatgggt ctgaaacatc aatataaagg tttgaatggc aaaaaaaaaa 730
 aaaaaaaaaa aaa 743

<210> 36
 <211> 140
 <212> PRT
 <213> Mesembryanthemum crystallinum

<400> 36
 Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu
 1 5 10 15
 Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg
 20 25 30
 Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg
 35 40 45
 Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser
 50 55 60
 Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val
 65 70 75 80

Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala
85 90 95

Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe
100 105 110

Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile
115 120 125

Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val
130 135 140

<210> 37
<211> 348
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (1)..(246)

<400> 37
atc att gct ccc cta gct att ggt ttg atc gtt ggt gcc aac atc tta 48
Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu
1 5 10 15

gcc gga ggt gca ttt gat ggt gcc tca atg aac cct gcc gtc tct ttt 96
Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
20 25 30

ggc ccc gcc gtg gtt agc tgg agc tgg gcc aac cac tgg gtc tac tgg 144
Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
35 40 45

gca ggc cca ctc att ggt ggt gga ctt gct ggt ctc gtt tat gag ttt 192
Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
50 55 60

atc ttt att ggt cac caa gag cca gct tcc gct gac tac cag aga ctc 240
Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu
65 70 75 80

tct gct taagaatttt aattctttgc cctagggaaa aatgtttcat gcatgtattt 296
Ser Ala

tggtattttg ttgggtctaa aattttatga agggaaaaaa aaaaaaaaaa aa 348

<210> 38
<211> 82
<212> PRT
<213> Sueada japonica

<400> 38

Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu
 1 5 10 15
 Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
 20 25 30
 Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
 35 40 45
 Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
 50 55 60
 Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu
 65 70 75 80
 Ser Ala

<210> 39
 <211> 1602
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (1)..(1419)

<400> 39
 cac acc gtt gat tta acc att gaa gct atg atg ctc gat tct caa gct 48
 His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala
 1 5 10 15
 tct gat ctt gac aaa gaa gaa cgt cct gag att ctt tca atg ctt ccg 96
 Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro
 20 25 30
 cct ctt gaa gga aaa tgc ctc ttg gaa ctt ggg gct ggt att ggt cgt 144
 Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg
 35 40 45
 ttt act ggt gaa ttg gct gag aaa gct ggc cag gtt att gct ctg gat 192
 Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp
 50 55 60
 ttc att gag agt gct atc aag aag aat gaa gta atc aat ggg cac tac 240
 Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr
 65 70 75 80
 aaa aat gtc aag ttt atg tgt gct gat gtg act tct ccc act ctc agt 288
 Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser
 85 90 95
 ttc cca cca cat tca ttg gat gtg ata ttc tcc aat tgg tta ctc atg 336
 Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met
 100 105 110

tat ctt tct gat gaa gag gtg gaa aat ttg gtt gaa aga atg ttg aaa	384
Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys	
115 120 125	
tggttg aag cca ggg ggt tac att ttc ttc aga gaa tct tgt ttc cat	432
Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His	
130 135 140	
caa tct ggg gat cac aaa cgc aaa agc aat ccc acc cac tac cgt gaa	480
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu	
145 150 155 160	
cct agg ttc tac act aag gcc ttc aaa gag tgt cat ttg caa gat gga	528
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly	
165 170 175	
tct gga aac tct tat gag ctc tcc cta ctt agc tgc aaa tgt att gga	576
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly	
180 185 190	
gct tat gtc aga aac aag aaa aac cag aac cag att agt tgg ttg tgg	624
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp	
195 200 205	
caa aaa gtt gat tct aag gat gat aag ggg ttc cag cga ttt ctg gat	672
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp	
210 215 220	
act agc cag tac aag tgt aat agc att ctg cga tat gag cgt gta ttt	720
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe	
225 230 235 240	
ggc cct ggt tat gtt agc act gga gga tat gaa acc acc aaa gag ttt	768
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe	
245 250 255	
gtg tca atg ctg gac ttg aag cct ggc cag aag gtc ctg gat gtt ggt	816
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly	
260 265 270	
tgt gga att ggt gga ggt gac ttt tac atg gcg gag acc ttt gat gtt	864
Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val	
275 280 285	
gag gtt gtt gga ttt gat ctc tcc gtt aat atg att tcc ttt gcc ctt	912
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu	
290 295 300	
gag cgt tct att ggg ctt aaa tgt gct gtt gag ttt gag gta gca gat	960
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp	
305 310 315 320	
tgc acc aag ata aac tac cct gat aac tct ttt gat gtc atc tat agc	1008
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser	
325 330 335	

cgt gac acc att ctg cat att cag gac aag cct gcg ttg ttt aga tcc	1056
Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser	
340 345 350	
ttc tac aaa tgg ttg aag cca gga ggt aaa gtt cta atc agt gat tac	1104
Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr	
355 360 365	
tgc aag aaa gct ggt cca ccc tca cct gaa ttc gcc gct tac att aag	1152
Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys	
370 375 380	
cag agg gga tat gat ctc cat gat gta aag gaa tat ggg cag atg ctt	1200
Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu	
385 390 395 400	
aaa gat gct gga ttt gtt gat gtt ctt gcc gag gat aga act gag cag	1248
Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln	
405 410 415	
ttc att cga gtt cta cgg aag gaa cta gag act gtt gag aag gaa aag	1296
Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys	
420 425 430	
gat gtg ttc att agt gat ttc tct gag gag gat tac aat gac att gtt	1344
Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val	
435 440 445	
gga ggt tgg aat gat aag ttg cgg agg act gcc aag ggt gag caa cga	1392
Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg	
450 455 460	
tgg ggt ctg ttc gtt gcc aag aag aag tgaagaatca gttgccgcac	1439
Trp Gly Leu Phe Val Ala Lys Lys Lys	
465 470	
tggcactgtc gatttcctag tattaatctt caatgttttc atgtaatgta cttctacatg	1499
taaaattgcc aataagttgc atttcgcaga ctgtaagatg attaatacata ttttatcttt	1559
taattaatca tggatttatg caaaaaaaaaa aaaaaaaaaa aaa	1602

<210> 40

<211> 473

<212> PRT

<213> Sueada japonica

<400> 40

His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala
1 5 10 15

Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro
20 25 30

Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg
35 40 45

Phe	Thr	Gly	Glu	Leu	Ala	Glu	Lys	Ala	Gly	Gln	Val	Ile	Ala	Leu	Asp		
50						55					60						
Phe	Ile	Glu	Ser	Ala	Ile	Lys	Lys	Asn	Glu	Val	Ile	Asn	Gly	His	Tyr		
65					70					75					80		
Lys	Asn	Val	Lys	Phe	Met	Cys	Ala	Asp	Val	Thr	Ser	Pro	Thr	Leu	Ser		
				85					90					95			
Phe	Pro	Pro	His	Ser	Leu	Asp	Val	Ile	Phe	Ser	Asn	Trp	Leu	Leu	Met		
			100					105					110				
Tyr	Leu	Ser	Asp	Glu	Glu	Val	Glu	Asn	Leu	Val	Glu	Arg	Met	Leu	Lys		
		115					120					125					
Trp	Leu	Lys	Pro	Gly	Gly	Tyr	Ile	Phe	Phe	Arg	Glu	Ser	Cys	Phe	His		
130						135					140						
Gln	Ser	Gly	Asp	His	Lys	Arg	Lys	Ser	Asn	Pro	Thr	His	Tyr	Arg	Glu		
145					150					155					160		
Pro	Arg	Phe	Tyr	Thr	Lys	Ala	Phe	Lys	Glu	Cys	His	Leu	Gln	Asp	Gly		
				165					170					175			
Ser	Gly	Asn	Ser	Tyr	Glu	Leu	Ser	Leu	Leu	Ser	Cys	Lys	Cys	Ile	Gly		
			180					185					190				
Ala	Tyr	Val	Arg	Asn	Lys	Lys	Asn	Gln	Asn	Gln	Ile	Ser	Trp	Leu	Trp		
		195					200					205					
Gln	Lys	Val	Asp	Ser	Lys	Asp	Asp	Lys	Gly	Phe	Gln	Arg	Phe	Leu	Asp		
210						215					220						
Thr	Ser	Gln	Tyr	Lys	Cys	Asn	Ser	Ile	Leu	Arg	Tyr	Glu	Arg	Val	Phe		
225					230					235					240		
Gly	Pro	Gly	Tyr	Val	Ser	Thr	Gly	Gly	Tyr	Glu	Thr	Thr	Lys	Glu	Phe		
				245					250					255			
Val	Ser	Met	Leu	Asp	Leu	Lys	Pro	Gly	Gln	Lys	Val	Leu	Asp	Val	Gly		
			260					265					270				
Cys	Gly	Ile	Gly	Gly	Gly	Asp	Phe	Tyr	Met	Ala	Glu	Thr	Phe	Asp	Val		
		275					280					285					
Glu	Val	Val	Gly	Phe	Asp	Leu	Ser	Val	Asn	Met	Ile	Ser	Phe	Ala	Leu		
	290					295					300						
Glu	Arg	Ser	Ile	Gly	Leu	Lys	Cys	Ala	Val	Glu	Phe	Glu	Val	Ala	Asp		
305					310					315					320		
Cys	Thr	Lys	Ile	Asn	Tyr	Pro	Asp	Asn	Ser	Phe	Asp	Val	Ile	Tyr	Ser		
				325					330					335			
Arg	Asp	Thr	Ile	Leu	His	Ile	Gln	Asp	Lys	Pro	Ala	Leu	Phe	Arg	Ser		
			340					345					350				

Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr
 355 360 365
 Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys
 370 375 380
 Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu
 385 390 395 400
 Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln
 405 410 415
 Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys
 420 425 430
 Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val
 435 440 445
 Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg
 450 455 460
 Trp Gly Leu Phe Val Ala Lys Lys Lys
 465 470

<210> 41
 <211> 1251
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (1) .. (933)

<400> 41
 cag cca ttt ggc aca att aat gga tca ctt cgt gtt act gta caa ggt 48
 Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
 1 5 10 15
 gag gtc att gaa caa tct ttt gga gag gag cac ttg tgt ttt aga aca 96
 Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
 20 25 30
 tta cag cgg tac aca gct gcc aca ctt gag cat gga atg cat cca cca 144
 Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
 35 40 45
 atc tct cct aaa cca gaa tgg cgt gca ctt ttg gac gag atg gct gtt 192
 Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
 50 55 60
 gtt gcc acc aag gaa tac cgc tct gtt gtt ttt cat gag cct cgc ttt 240
 Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
 65 70 75 80

gtc gag tac ttc cgc agt gct aca cca gag aca gag tat ggg cgt atg	288
Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met	
85 90 95	
aat att gga agc cgt cct gca aag aga aag cca gga gga gga att gaa	336
Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu	
100 105 110	
act ctg cgt gca att cct tgg ata ttt tcg tgg aca caa acc agg ttt	384
Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe	
115 120 125	
cat tta cct gtg tgg ctt ggg gtt gga gca gct ttt aag cat gcc ctt	432
His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu	
130 135 140	
gac aag gac att aag aat ctt tcg ata ctc aag gcc atg tat aat gag	480
Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu	
145 150 155 160	
tgg ccg ttc ttc aga gtg act att gat ctc tta gaa atg gtt ttc act	528
Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr	
165 170 175	
aaa gga gac cct gga att gct gct tta tat gac aag ctt ctg gtg gca	576
Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala	
180 185 190	
gag gat ttg aag ccc ttt ggg gaa aag ttg agg aaa agt ttc gaa gat	624
Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp	
195 200 205	
acc aaa ctc ctt ctc ctt aag gtt gct ggg cac aag gag tta ctg gaa	672
Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu	
210 215 220	
gga gat cct tac ttg aaa cag aga ctc cga ctt cgt gat cct tac att	720
Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile	
225 230 235 240	
aca acc ctt aat gtt ttc caa gca tat act ctg aag cgg atc cgt gat	768
Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp	
245 250 255	
ccc aat ttc cat gta gct gaa ggg cca cac tta tcc aag gaa gta ttg	816
Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu	
260 265 270	
gaa tca aac aat gct gag ctt gtg aag ctc aat cct act agt gag tat	864
Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr	
275 280 285	
cct cct ggc ctt gag gac acc ctt atc ttg acc atg aag ggt att gct	912
Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala	
290 295 300	
gct ggc atg cag aac acc ggt taactgacac gtgttgacacg tctattgcaa	963

Ala Gly Met Gln Asn Thr Gly
305 310

ctattcctca actccttctg gtttggggat ccgggctcgg agatagccat cgttgggtgat 1023
gtgctgtatg agcacctaata tgtattcaaaa gtctgtattt caagtctatt gtatttgtat 1083
tttgttcttc tgtatgtttt tgttatttct acttatgggtt gggttgtgtc acttgtgact 1143
aatacccgac tgtgtaataa atgggttggtg tactgatgaa cagtttgttt tcttctacgt 1203
gagttatatt gatgagttta tcttttatta aaaaaaaaaa aaaaaaaaaa 1251

<210> 42
<211> 311
<212> PRT
<213> Salsola komarovii

<400> 42
Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
1 5 10 15
Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
20 25 30
Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
35 40 45
Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
50 55 60
Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
65 70 75 80
Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
85 90 95
Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu
100 105 110
Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
115 120 125
His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu
130 135 140
Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu
145 150 155 160
Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr
165 170 175
Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala
180 185 190
Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp

195						200						205					
Thr	Lys	Leu	Leu	Leu	Leu	Lys	Val	Ala	Gly	His	Lys	Glu	Leu	Leu	Glu		
210						215						220					
Gly	Asp	Pro	Tyr	Leu	Lys	Gln	Arg	Leu	Arg	Leu	Arg	Asp	Pro	Tyr	Ile		
225						230						235		240			
Thr	Thr	Leu	Asn	Val	Phe	Gln	Ala	Tyr	Thr	Leu	Lys	Arg	Ile	Arg	Asp		
				245						250				255			
Pro	Asn	Phe	His	Val	Ala	Glu	Gly	Pro	His	Leu	Ser	Lys	Glu	Val	Leu		
		260						265				270					
Glu	Ser	Asn	Asn	Ala	Glu	Leu	Val	Lys	Leu	Asn	Pro	Thr	Ser	Glu	Tyr		
		275						280				285					
Pro	Pro	Gly	Leu	Glu	Asp	Thr	Leu	Ile	Leu	Thr	Met	Lys	Gly	Ile	Ala		
290						295						300					
Ala	Gly	Met	Gln	Asn	Thr	Gly											
305						310											

<210> 43
 <211> 637
 <212> DNA
 <213> Avicennia marina

<220>
 <221> CDS
 <222> (1) .. (339)

<400> 43																
caa	tac	ttg	gta	aat	gaa	gtg	aag	aaa	act	gtt	cag	ggg	cgt	gct	caa	48
Gln	Tyr	Leu	Val	Asn	Glu	Val	Lys	Lys	Thr	Val	Gln	Gly	Arg	Ala	Gln	
1				5					10					15		
ctt	ggt	gtg	gaa	gca	ttt	gct	gat	gcg	ctt	ctt	gtg	gtt	cca	aag	acg	96
Leu	Gly	Val	Glu	Ala	Phe	Ala	Asp	Ala	Leu	Leu	Val	Val	Pro	Lys	Thr	
			20					25					30			
ctt	gcc	gag	aac	tct	ggc	ctt	gat	acc	cag	gat	ttg	att	att	gaa	ctt	144
Leu	Ala	Glu	Asn	Ser	Gly	Leu	Asp	Thr	Gln	Asp	Leu	Ile	Ile	Glu	Leu	
			35					40				45				
acg	gga	gaa	tat	gaa	aaa	ggg	aat	gtg	gta	gga	ctt	aat	cta	cac	aca	192
Thr	Gly	Glu	Tyr	Glu	Lys	Gly	Asn	Val	Val	Gly	Leu	Asn	Leu	His	Thr	
	50					55					60					
gga	gaa	cct	ata	gat	cct	caa	atg	gag	ggg	atc	ttt	gac	aat	tat	tcc	240
Gly	Glu	Pro	Ile	Asp	Pro	Gln	Met	Glu	Gly	Ile	Phe	Asp	Asn	Tyr	Ser	
65					70					75					80	
gtg	aag	cgt	cag	atc	ata	aac	tca	ggc	ccc	gtt	att	gca	tct	cag	ctg	288
Val	Lys	Arg	Gln	Ile	Ile	Asn	Ser	Gly	Pro	Val	Ile	Ala	Ser	Gln	Leu	

85	90	95	
cta ctt gtc gac gag gtt att cgt gct ggt cgt aac atg cgt aaa ccg			336
Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro			
100	105	110	
aat tagctttcac cctagttttt gtgatgttgg tgaagatggg aattttatatt			389
Asn			
aggtaggggtc atgggttcctt ttgttttagcc taagcactat gtattcattg ccacttgaga			449
tttgaatttt gatcatcagg cggttgaact tttcgctgt tacaaaattgc accagaaatt			509
attcgaccat gggtatgcat ctacttgtgt tgtacctgac ttggctaagt tatttgaaga			569
tacactctgt gctcagcaaa gaattggaaa aaaaggaatt gatttcatca aaaaaaaaaa			629
aaaaaaaa			637

<210> 44
 <211> 113
 <212> PRT
 <213> Avicennia marina

<400> 44															
Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln															
1			5				10						15		
Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr															
		20				25						30			
Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu															
		35				40					45				
Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr															
		50				55					60				
Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser															
		65				70				75				80	
Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu															
				85				90					95		
Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro															
		100					105					110			
Asn															

<210> 45
 <211> 741
 <212> DNA
 <213> Avicennia marina

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<220>
<221> CDS
<222> (3)..(293)

<400> 45
aa gag atc aat tgt ctt gaa tgg gag aac ttt gct ttc cat ccc agc 47
   Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser
      1             5             10             15

cca ctc att gtt ctt gtt ttt gaa aga tac aac agg gca agt gat aac 95
Pro Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn
      20             25             30

tgg aaa gct ttg aag gag ttg gaa aag gcg gca gaa gtt tac tgg aag 143
Trp Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys
      35             40             45

gca aaa gat cga ctg cct cct cgg acg gtc aag ata gat ata aac atc 191
Ala Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile
      50             55             60

gaa agg gat tta gca tat gca ctc aag gtt aaa gaa tgc ccg cag ata 239
Glu Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile
      65             70             75

ctg ttc tta cgc gga aac agg ata tta tac aga gag aaa ggt agc cca 287
Leu Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro
      80             85             90             95

ttt ctc tgatattgca tgtacatcag atctttcaat ctgcaccaga accaattgag 343
Phe Leu

tttaccatca tttccagaaa ttagatcatc ggatgaattg gttcagatga tcgcgcattt 403

ctattacaat gcaaaaaagc cttcgtgcat cgatgatgca gcttttctctt caccacatca 463

ctgaagggtga ggttgtcaaaa tggaatccag catcagtcac tagggaggagac tgaagctgta 523

cggagggaag tggtttaaat tcagattgga tctttgaagt gggcagtggt gattgaaacg 583

ccaaaagtgt ctgaggaata accttggttg gattttgcag tgaactgtag taactttctc 643

gcatgtaaaa ctagactttc atcaatcaac caccaaccct tttatgtata tgaaacctat 703

gagggtgaaa tttctagtta aaaaaaaaaa aaaaaaaaaa 741

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<210> 46
<211> 97
<212> PRT
<213> Avicennia marina

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<400> 46
Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser Pro
 1             5             10             15

Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn Trp

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Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys Ala
35 40 45

Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile Glu
50 55 60

Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile Leu
65 70 75 80

Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro Phe
,P

,R,Q□^,X,P

85

90

95

Leu

<210> 47

<211> 983

<212> DNA

<213> *Salsola komarovii*

<220>

<221> CDS

<222> (1) .. (762)

<400> 47

atg ttc ctt cat cac cac ttt tca tct tca tct tct tct ttt ctt ctt	48
Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu	
1 5 10 15	
ctc ttc ttc tct ctc cta ata ttc ctt tca tct gct aat ctt tat cat	96
Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His	
20 25 30	
cag aat caa gga tct tgt agt gac ttt gaa tca gaa cca tca atg gct	144
Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala	
35 40 45	
act ctt ggt gga ttg cgc gaa tcc cat ggt gct tct aat gat gct gag	192
Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu	
50 55 60	
att gaa acc ctt gct cgc ttt gct gtt gat gaa cac aac aaa aaa gag	240
Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu	
65 70 75 80	
aat gca ttg ttg gag ttt gca agg gtt gta aag gca aag gaa cag gtg	288
Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val	
85 90 95	
gtt gcg ggt aca ttg cat cac ttc act atc gaa gca att gaa gcg ggc	336
Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly	
100 105 110	
aag aag aag ctc tac gaa gcg aag gtg tgg gtg aag cca tgg atg aac	384
Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn	
115 120 125	
ttt aag gag ctg cag gaa ttt aag cat gct gat gaa tcc cct tca atc	432
Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile	
130 135 140	
act cct tcc gac ctc ggc gct aat aga gaa ggg cat tct gga gga tgg	480
Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp	
145 150 155 160	

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aaa gat gtg cct gtc cat gac cct gaa gtg caa aat gca gca aat cat 528
Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His
165 170 175

gct ctt aag acc ttg caa caa aga tcc aac tcc tta ttt cct tat gaa 576
Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu
180 185 190

ctg cag gaa gtt gct cat gct agg gct gag gtt ctg gaa gac act gcg 624
Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala
195 200 205

aag ttt aac ctg cac ctc aag gtg aag aga gga aac aag gat gag ttt 672
Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe
210 215 220

ttc aat gtg gag gtg cac aaa aac agc gaa gga aac tac aac ctt aat 720
Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
225 230 235 240

cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt 762
Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
245 250

tagactcggt gaggggtgttg taagtactcg ttcgtaactt ttctgatggg caggcaagta 822

tgtagtaagg actagactac tagtactagt aagtacagct gacttggttt gagtaaaata 882

acctcgactt tgggtgcacc atcatatctt gtatgtttat ggctttgtca atgtattgta 942

agtgaagatt gtttgcttga tctaaaaaaaa aaaaaaaaaa a 983

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<210> 48
<211> 254
<212> PRT
<213> Salsola komarovii

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<400> 48
Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu
1 5 10 15

Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His
20 25 30

Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala
35 40 45

Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu
50 55 60

Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu
65 70 75 80

Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val
85 90 95

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Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly
 100 105 110
 Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn
 115 120 125
 Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile
 130 135 140
 Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp
 145 150 155 160
 Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His
 165 170 175
 Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu
 180 185 190
 Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala
 195 200 205
 Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe
 210 215 220
 Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
 225 230 235 240
 Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
 245 250

<210> 49
 <211> 543
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (3)..(389)

<400> 49
 aa aat aag gtt gac tta gct cga gat ttc acc ttc ata gac gac gtc 47
 Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val
 1 5 10 15
 gta aag ggg tgc tta ggt tca ctg gat tct tcc ggt aag agt acc ggt 95
 Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly
 20 25 30
 agc ggc ggt aaa aaa cgt ggg ccc gct ccg tac aga atc tac aac ttg 143
 Ser Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu
 35 40 45
 ggg aac act caa ccg gtc act gta ccg aca ctt gtc ggt atc cta gag 191
 Gly Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu
 50 55 60

aag cat ctc aaa gtt aag gcc aag aag aat gtg gtt gag atg ccc gga 239
 Lys His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly
 65 70 75

aat ggt gac gtg ccc ttc aca cat gcg aat atc tct ttg gcc cga aaa 287
 Asn Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys
 80 85 90 95

gat ttc ggg tat aaa ccc act acc gat ttg caa acc ggg ttg aaa aag 335
 Asp Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys
 100 105 110

ttt gtt aga tgg tat ctc act tat tac ggc tac aac aac ggc aag cct 383
 Phe Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro
 115 120 125

gta aat taatatataa atataagtaa tattttttttt ctctttttttt ataaattaca 439
 Val Asn

gaattattttt ttttgggtgg tttatgaatt ttgttgata atatggggat tcttttttttc 499

taaatgggaa aaataagaat ccaaggaaaa aaaaaaaaaa aaaa 543

<210> 50

<211> 129

<212> PRT

<213> Salsola komarovii

<400> 50

Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val Val
 1 5 10 15

Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly Ser
 20 25 30

Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu Gly
 35 40 45

Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu Lys
 50 55 60

His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly Asn
 65 70 75 80

Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys Asp
 85 90 95

Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys Phe
 100 105 110

Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro Val
 115 120 125

Asn

<210> 51
<211> 1219
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (2) .. (871)

<400> 51

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c aca gga gca aac aaa gga ata gga ctt gaa cta tgc aaa caa cta gct 49
  Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
    1             5             10             15

gct aaa gga gtt gta gta gtt ctc act tct aga gat gga aaa aga ggc 97
Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
      20             25             30

tta caa gct cat gaa aat ctc att aaa tct gga att aat cct gaa aat 145
Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
      35             40             45

ctt cac ttt cat cag ctc gat gtt act gac atc act agt att gct gct 193
Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
      50             55             60

att gct ggt ttc atc aat tcc aaa ttc ggc aaa ctt gat atc ctg gtg 241
Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
      65             70             75             80

aac aat gct gga att att gga gat atg gtt aac ttt gat gct tta ata 289
Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
      85             90             95

gca gca gga ttt ggc act cca aga gaa cag atc aat ctt gag gac agt 337
Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
      100            105            110

ccc ggg aca gta aca cag aca tat gag ctt acg aaa gaa tgc tta caa 385
Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
      115            120            125

aca aat tat tat gga gcg aaa aga acc gtt gaa gct ttg ctt ccg ctt 433
Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
      130            135            140

ctc aag tta tcc gat tct cca agg att gtc aat gtc tcc tct ttt cta 481
Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu
      145            150            155            160

gga agg ttg acg tat ata cca aat gag acg atc aga ggg gtc cta aga 529
Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
      165            170            175
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gat gcc gag agc ctt aca gaa gaa cga ata gat gag att ctg aat gac 577
Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp
180 185 190

atg ctg agg gac ttc aaa gac tgt tca ttc aaa gag aag gga tgg cct 625
Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro
195 200 205

aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac 673
Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr
210 215 220

aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att 721
Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile
225 230 235 240

tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg 769
Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu
245 250 255

ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc 817
Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro
260 265 270

caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg 865
Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser
275 280 285

ttt gaa taaaacaatt tgcctattca aaccaacacc acatatctat gaagtttcca 921
Phe Glu
290

tttgtaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa 981

tgtacttttt tcatgtatgc atggcgcagt tattttattct gactgcaaca ataagattct 1041

gttctttcaa ggcaactctaa ggaatgctga tgtaccgttc tcaaacaagc agacaagtag 1101

acacgtttga ttgtcatgtc ttcattcgta caatcatttt gtgtttgtat gttgagcatg 1161

tttaactaat tacaagagtg taattaagat caacttttat aaaaaaaaaa aaaaaaaaaa 1219

<210> 52

<211> 290

<212> PRT

<213> Sueada japonica

<400> 52

Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
1 5 10 15

Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
20 25 30

Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
35 40 45

Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
 50 55 60
 Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
 65 70 75 80
 Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
 85 90 95
 Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
 100 105 110
 Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
 115 120 125
 Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
 130 135 140
 Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu
 145 150 155 160
 Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
 165 170 175
 Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp
 180 185 190
 Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro
 195 200 205
 Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr
 210 215 220
 Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile
 225 230 235 240
 Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu
 245 250 255
 Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro
 260 265 270
 Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser
 275 280 285
 Phe Glu
 290

<210> 53
 <211> 1148
 <212> DNA
 <213> Sueada japonica

<220>

<221> CDS

<222> (3)..(848)

<400> 53

ga agc agg ccg gat atc cat gtt gaa caa gct cat tca gat gat att	47
Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile	
1 5 10 15	
act ggg ttg aaa ttc tca tgt gat ggt cgt cat ctg ttg tct aga agt	95
Thr Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser	
20 25 30	
ttt gat tgc aca ctt aag gtt tgg gac ttg cgc caa atg aag cgg tct	143
Phe Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser	
35 40 45	
ctt aag gtg ttt gat gaa tta cca aat cac tat gct caa acg aat gtc	191
Leu Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val	
50 55 60	
tca ttt agt cca gat gag cag ctc atc ttg act ggt aca tct gta gaa	239
Ser Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu	
65 70 75	
agg gat agc cca act gga gga ttg ttg tgc ttt tat gat cgg gaa aaa	287
Arg Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys	
80 85 90 95	
ctt gaa cta gta tca aaa gtt ggc att tct cct act tgc agt gtt gtg	335
Leu Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val	
100 105 110	
caa tgt gcc tgg cac cca agg ctg aat cag gtt ttt gcc act gct gga	383
Gln Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly	
115 120 125	
aat aaa agc caa gga ggt aca cat gta ctc tat gat cca acc atg agt	431
Asn Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser	
130 135 140	
gag aga ggt gct ctt gtg tgt gtt gct cgt gca cca agg atg aaa tca	479
Glu Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser	
145 150 155	
gtg gat gat ttt gag gtg cag ccg gtt ata cat aac cct cac gca ctt	527
Val Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu	
160 165 170 175	
ccc ttg ttc aga gat cag cca agc cgc aaa cgt caa aga gag aag att	575
Pro Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile	
180 185 190	
ctg aag gac cca ata aaa tcc cac aaa cca gag ctt cct atg tca gga	623
Leu Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly	
195 200 205	
cct ggc cat ggt ggc aga act ggt aca tca tcg ggt agt ttg tta aca	671

Pro Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr
 210 215 220
 caa tat ctc ctc aag caa ggg ggc atg ttg aaa gag aca tgg atg gat 719
 Gln Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp
 225 230 235
 gaa gat ccc aga gaa gct att ctc aag tat gct gat gct gca gaa aag 767
 Glu Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys
 240 245 250 255
 gat cca aag ttt att gcc ccg gct tat gct gag act cag ccc aag cca 815
 Asp Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro
 260 265 270
 gtc ttt gag gat tct gat aag gaa gat gaa gaa taattcatct tttgcagtgg 868
 Val Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu
 275 280
 ttggattaat ttaatttgag aatattatac tgtgtatatt aatagccaat ttttcaggcg 928
 aatgatatgc ttctcacatt acatgctgag ttttatttgc tgctacagat tgtagatgaa 988
 taggttaatg taaacacaag catagagatt agaatataga aatgattctg tatccaaaac 1048
 acaattttat caccagatgg tatcaaaagc tgtattgact gttgagtaat gtcattaacc 1108
 acttttcactc cccaaaaaaa aaaaaaaaaa aaaaaaaaaa 1148

<210> 54
 <211> 282
 <212> PRT
 <213> Sueada japonica

<400> 54
 Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile Thr
 1 5 10 15
 Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser Phe
 20 25 30
 Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser Leu
 35 40 45
 Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val Ser
 50 55 60
 Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu Arg
 65 70 75 80
 Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys Leu
 85 90 95
 Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val Gln
 100 105 110

Cys	Ala	Trp	His	Pro	Arg	Leu	Asn	Gln	Val	Phe	Ala	Thr	Ala	Gly	Asn	
	115						120					125				
Lys	Ser	Gln	Gly	Gly	Thr	His	Val	Leu	Tyr	Asp	Pro	Thr	Met	Ser	Glu	
	130					135					140					
Arg	Gly	Ala	Leu	Val	Cys	Val	Ala	Arg	Ala	Pro	Arg	Met	Lys	Ser	Val	
145					150					155					160	
Asp	Asp	Phe	Glu	Val	Gln	Pro	Val	Ile	His	Asn	Pro	His	Ala	Leu	Pro	
			165					170						175		
Leu	Phe	Arg	Asp	Gln	Pro	Ser	Arg	Lys	Arg	Gln	Arg	Glu	Lys	Ile	Leu	
		180						185					190			
Lys	Asp	Pro	Ile	Lys	Ser	His	Lys	Pro	Glu	Leu	Pro	Met	Ser	Gly	Pro	
	195						200					205				
Gly	His	Gly	Gly	Arg	Thr	Gly	Thr	Ser	Ser	Gly	Ser	Leu	Leu	Thr	Gln	
	210					215					220					
Tyr	Leu	Leu	Lys	Gln	Gly	Gly	Met	Leu	Lys	Glu	Thr	Trp	Met	Asp	Glu	
225					230					235					240	
Asp	Pro	Arg	Glu	Ala	Ile	Leu	Lys	Tyr	Ala	Asp	Ala	Ala	Glu	Lys	Asp	
			245						250					255		
Pro	Lys	Phe	Ile	Ala	Pro	Ala	Tyr	Ala	Glu	Thr	Gln	Pro	Lys	Pro	Val	
		260						265					270			
Phe	Glu	Asp	Ser	Asp	Lys	Glu	Asp	Glu	Glu							
	275						280									

<210> 55
 <211> 1193
 <212> DNA
 <213> Avicennia marina

<220>
 <221> CDS
 <222> (3) .. (815)

<400> 55																
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	Ala	Pro	Glu	Leu	Leu	Leu	Gly	Ala	Lys	His	Tyr	Thr	Ser	Ala	Val	
	1				5					10					15	
gac	atg	tgg	gct	gtg	ggc	tgc	att	ttt	gct	gag	ctt	ctg	act	cta	aag	95
Asp	Met	Trp	Ala	Val	Gly	Cys	Ile	Phe	Ala	Glu	Leu	Leu	Thr	Leu	Lys	
			20						25					30		
cca	cta	ttt	caa	ggg	caa	gaa	gta	aaa	ggg	act	tct	aat	cca	ttt	cag	143
Pro	Leu	Phe	Gln	Gly	Gln	Glu	Val	Lys	Gly	Thr	Ser	Asn	Pro	Phe	Gln	
			35					40					45			

ctt gat caa ctt gac aaa atc ttt aag gtc cta ggt cat ccc acg caa	191
Leu Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln	
50 55 60	
gaa aag tgg ccc aca cta gcg aat ctt cca cat tgg cag tct gat gtg	239
Glu Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val	
65 70 75	
caa cgt atc caa ggg ctc aaa tac gac aat act gga ctt tac aat gtt	287
Gln Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val	
80 85 90 95	
gtt cat ctc tcc ccc aaa aat cca gca tat gac ctt ctc tca aag atg	335
Val His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met	
100 105 110	
ctt gag tat gat cct aga aaa aga ata aca gct aca caa gct ctt gag	383
Leu Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu	
115 120 125	
cat gag tat ttt cgc atg gaa cct ttg ccg gga cgc aac gct ctg gta	431
His Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val	
130 135 140	
cca cca cag cct ggg gag aaa att gtg aac tac cca aca cga cca gtg	479
Pro Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val	
145 150 155	
gac aca aat act gat att gaa gga aca atc agc ctc cag ccc tct caa	527
Asp Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln	
160 165 170 175	
ccg gta tca tct ggg aat tct gtg tct ggg gcc cta gcc ggt cct cat	575
Pro Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His	
180 185 190	
gta atg caa aat aga tcc atg cct cgg cca atg ccc atg gtt ggc gtg	623
Val Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val	
195 200 205	
caa cgc atg caa cct cca ggg atc cca cac tat ggt ctt gct tct cag	671
Gln Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln	
210 215 220	
gca gga atg ggt gga gta aat cct ggt ggc atc cca att cag cgg gga	719
Ala Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly	
225 230 235	
gtt cct gct cag gct cat caa cag cag cag atg aga agg aaa gac cct	767
Val Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro	
240 245 250 255	
gga atg ggg atg act gga tat cct cca caa cag aaa tca agg cgc ttt	815
Gly Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe	
260 265 270	
tgagagtcgg ggtggatttg gagcctaagt gggaggacaa atacacattc caatcaaatt	875

agaggaaacc ttaaattaat cttccagtca gctgaaacga caccagtgga accaaatgat 935
 ctgaccccat ttccaggatt gcatgtatatt attaggagga atacacgaat gaagattcga 995
 gtctagtgcc aaattattct aacatacctt catcatttgt tcctactaca ttccgacgtt 1055
 atatgtttca actagtggaa gggtttctgc agtccacca tgtggcacia acatgattca 1115
 tagcatgcca agcaacactt tactgggtgtg taccaaggca atttctctat ttccaagcca 1175
 aaaaaaaaaa aaaaaaaaaa 1193

<210> 56
 <211> 271
 <212> PRT
 <213> Avicennia marina

<400> 56
 Ala Pro Glu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val Asp
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 Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys Pro
 20 25 30
 Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln Leu
 35 40 45
 Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln Glu
 50 55 60
 Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val Gln
 65 70 75 80
 Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val Val
 85 90 95
 His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met Leu
 100 105 110
 Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu His
 115 120 125
 Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val Pro
 130 135 140
 Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val Asp
 145 150 155 160
 Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln Pro
 165 170 175
 Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His Val
 180 185 190
 Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val Gln

195					200					205						
Arg	Met	Gln	Pro	Pro	Gly	Ile	Pro	His	Tyr	Gly	Leu	Ala	Ser	Gln	Ala	
210					215					220						
Gly	Met	Gly	Gly	Val	Asn	Pro	Gly	Gly	Ile	Pro	Ile	Gln	Arg	Gly	Val	
225					230					235					240	
Pro	Ala	Gln	Ala	His	Gln	Gln	Gln	Gln	Met	Arg	Arg	Lys	Asp	Pro	Gly	
245					250					255						
Met	Gly	Met	Thr	Gly	Tyr	Pro	Pro	Gln	Gln	Lys	Ser	Arg	Arg	Phe		
260					265					270						

<210> 57
 <211> 1195
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (116) .. (1195)

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 atagtggcaa aacaatagag ggcaaattct cattgcccaa ttcaaatttg gtaaa atg 118
 Met
 1
 gct caa aag cat ttg aaa gaa ctt ctc aaa gaa gat caa gaa ccc ttt 166
 Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro Phe
 5 10 15
 cat tta aag gat tac att gca act aaa aaa tgt caa ctt ttg aag aag 214
 His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys Lys
 20 25 30
 caa gaa tta gta gta ccc aaa tca aaa ctt caa ctc aaa aag cca aag 262
 Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro Lys
 35 40 45
 cca aaa cca att tca aaa agc act tca gtt ttg tgc aaa aat gct tgc 310
 Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala Cys
 50 55 60 65
 ttt tta tct tta caa gaa tcc cct gac ctc aga aaa tcc ccc aaa cta 358
 Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys Leu
 70 75 80
 ttt gat ttt cca cct tcc cct gtt tct aac aaa agc cca aac aga gta 406
 Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg Val
 85 90 95
 ttc ctc aat gtt cct gct aaa act gct gct ctt ctt ctt gaa gct gct 454

Phe	Leu	Asn	Val	Pro	Ala	Lys	Thr	Ala	Ala	Leu	Leu	Leu	Glu	Ala	Ala		
		100					105						110				
att	cga	att	caa	acc	cac	aaa	tct	aaa	ccc	aaa	acc	cag	att	aaa	aat	502	
Ile	Arg	Ile	Gln	Thr	His	Lys	Ser	Lys	Pro	Lys	Thr	Gln	Ile	Lys	Asn		
	115					120					125						
tcg	ggg	ttt	ggg	cta	ttc	ggg	tca	atg	tta	aag	cga	tta	aat	ctt	cga	550	
Ser	Gly	Phe	Gly	Leu	Phe	Gly	Ser	Met	Leu	Lys	Arg	Leu	Asn	Leu	Arg		
130					135					140					145		
aat	cgt	acc	caa	aaa	atc	aag	tca	aaa	aca	gag	gaa	caa	aac	aga	gga	598	
Asn	Arg	Thr	Gln	Lys	Ile	Lys	Ser	Lys	Thr	Glu	Glu	Gln	Asn	Arg	Gly		
			150						155					160			
tgc	tct	gtt	ttg	agg	agt	gtt	gaa	gaa	gaa	aaa	act	acc	acc	att	tct	646	
Cys	Ser	Val	Leu	Arg	Ser	Val	Glu	Glu	Glu	Lys	Thr	Thr	Thr	Ile	Ser		
		165					170						175				
tct	tct	tca	tct	tca	tct	tct	tca	aca	tca	tcg	tat	tct	tcg	tgt	tct	694	
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Ser	Tyr	Ser	Ser	Cys	Ser		
		180					185					190					
tgc	aat	gag	agg	tta	agt	agt	ttg	gat	ttg	gag	agt	tct	agc	agt	gga	742	
Cys	Asn	Glu	Arg	Leu	Ser	Ser	Leu	Asp	Leu	Glu	Ser	Ser	Ser	Ser	Gly		
	195					200					205						
aga	tca	tta	cat	gat	gaa	gat	gaa	gat	gaa	gat	gaa	gat	gat	gaa	ttt	790	
Arg	Ser	Leu	His	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Asp	Glu	Phe		
210					215				220						225		
gag	ttt	aca	aat	gtt	tta	aga	gaa	aat	aat	aat	gat	gat	aaa	aat	gga	838	
Glu	Phe	Thr	Asn	Val	Leu	Arg	Glu	Asn	Asn	Asn	Asp	Asp	Lys	Asn	Gly		
			230					235						240			
ggg	tat	tat	tca	gga	att	tgc	tta	agt	cct	ttg	agt	cca	ttt	cgt	ttt	886	
Gly	Tyr	Tyr	Ser	Gly	Ile	Cys	Leu	Ser	Pro	Leu	Ser	Pro	Phe	Arg	Phe		
			245					250					255				
gct	ctt	cat	aaa	aac	tct	tct	cct	gaa	cgt	tgc	tct	cct	gct	aaa	tcc	934	
Ala	Leu	His	Lys	Asn	Ser	Ser	Pro	Glu	Arg	Cys	Ser	Pro	Ala	Lys	Ser		
		260					265					270					
cct	gtt	cgt	tgc	aaa	ttt	gag	ggg	aat	gct	aaa	tat	gaa	caa	gaa	agc	982	
Pro	Val	Arg	Cys	Lys	Phe	Glu	Gly	Asn	Ala	Lys	Tyr	Glu	Gln	Glu	Ser		
	275					280					285						
tta	ata	aag	ttt	gaa	gac	gaa	gat	gaa	gaa	gac	aaa	gag	caa	aat	agc	1030	
Leu	Ile	Lys	Phe	Glu	Asp	Glu	Asp	Glu	Glu	Asp	Lys	Glu	Gln	Asn	Ser		
290				295					300						305		
cct	gtt	tcc	gtg	ctc	gat	cct	cca	ttc	gag	gat	gat	tac	gat	ggg	cat	1078	
Pro	Val	Ser	Val	Leu	Asp	Pro	Pro	Phe	Glu	Asp	Asp	Tyr	Asp	Gly	His		
			310						315					320			
gag	gag	gat	agc	tac	gag	gac	atc	gaa	tgc	agc	tat	gct	ttt	gta	caa	1126	
Glu	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Glu	Cys	Ser	Tyr	Ala	Phe	Val	Gln		

325	330	335	
aga gca caa caa gag tta ttg cac	aga ctt cac cgg ttc cag aag cta	1174	
Arg Ala Gln Gln Glu Leu Leu His	Arg Leu His Arg Phe Gln Lys Leu		
340	345	350	

gcg gag ttg gac cca att gaa	1195
Ala Glu Leu Asp Pro Ile Glu	
355	360

<210> 58
 <211> 360
 <212> PRT
 <213> Sueada japonica

<400> 58	
Met Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro	
1 5 10 15	
Phe His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys	
20 25 30	
Lys Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro	
35 40 45	
Lys Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala	
50 55 60	
Cys Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys	
65 70 75 80	
Leu Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg	
85 90 95	
Val Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala	
100 105 110	
Ala Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys	
115 120 125	
Asn Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu	
130 135 140	
Arg Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg	
145 150 155 160	
Gly Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile	
165 170 175	
Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys	
180 185 190	
Ser Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser	
195 200 205	
Gly Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu	

210	215	220
Phe Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn		
225	230	235 240
Gly Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg		
	245	250 255
Phe Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys		
	260	265 270
Ser Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu		
	275	280 285
Ser Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn		
	290	295 300
Ser Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly		
305	310	315 320
His Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val		
	325	330 335
Gln Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys		
	340	345 350
Leu Ala Glu Leu Asp Pro Ile Glu		
	355	360

<210> 59
 <211> 1301
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (3) .. (815)

<400> 59	
gt gag gtt gac gat agc gtt aat agt cta cag gca gat gtt gac aac	47
Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn	
1 5 10 15	
ctt tca att gag gaa cgc aga ttg gat gaa cag ata agg gaa atg caa	95
Leu Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln	
20 25 30	
gaa aga ttg agg gaa atg agt gaa gat gat atc aat cag aag tgg ctt	143
Glu Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu	
35 40 45	
ttt gta act gaa gaa gac ata aag ggt tta cct tgt ttt cag aat gaa	191
Phe Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu	
50 55 60	

acc tta att gca att aaa gct cca cat gga aca act ttg gag gtt cca	239
Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro	
65 70 75	
gat cca gat gag gct gtc gat tat cct caa aga aga tac aag ata gtt	287
Asp Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val	
80 85 90 95	
ctt agg agc aca atg ggt cct att gat gta tat tta gtc agt caa ttt	335
Leu Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe	
100 105 110	
gaa gag aag ttt gag gag atc agt ggt gct gac ggt cca cta agt ata	383
Glu Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile	
115 120 125	
cca agt acc tca ggt gat gac aaa cac aca act gtt gca gct aag gaa	431
Pro Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu	
130 135 140	
gaa agc aat ggc aat gag att gaa ata gaa gga caa ggg acc cat aga	479
Glu Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg	
145 150 155	
atc tgc tca gat tcc aac gct cag caa gac ttt gtg agt gga att atg	527
Ile Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met	
160 165 170 175	
aag ata gtg cct gaa gtt gat agt gat gca gat tac tgg ttg cta tcg	575
Lys Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser	
180 185 190	
gat gct gat gtt agc att act gac atg tgg gga act gat tct gga gtt	623
Asp Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val	
195 200 205	
gaa tgg aat gaa tta ggg act ata cat gaa gac tat gcc gtg gct aat	671
Glu Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn	
210 215 220	
gtt ggc act tca cag cca caa agt cca cca aca agt gca aca gaa gtg	719
Val Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val	
225 230 235	
ctt cca gct aac atg aca agc agg aga ttg aca tgg agt ttt gag aga	767
Leu Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg	
240 245 250 255	
att gcc aar att cat tca aat ggt cac tat tgc ttg gaa gtg agg ctc	815
Ile Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu	
260 265 270	
taacttttcta ttattcatcc tgggatttgg gtacgaaagt ctgccttgaa gatgctgtaa	875
catgttgtgt attacaactg tgtgaatcta gtaagttggg agggtgagat tgttcctgat	935
cttattgcac agccggttgg gagagattga tcgctcaaca actgacaaaa ttggggcatg	995

ttaacggata gtagcgagtt gtaattttgt acatcacatt tgttgatttt agtcagtaca 1055
 tcataactag ctcttcctat acttcttcaa ttgtcaactg gaatagattt ttagattaat 1115
 tagatctctc tttgtatgga aatgtttcag ggtaacaagc cagaaattaa aatgggtttta 1175
 tgtgtaaaaa tatatactta aattgtttgt aggaagtttc tgatggggtg ttggatggct 1235
 tttacaact acatcgata aggaaattcg tatcacaat tcacaatgaa aaaaaaaaaa 1295
 aaaaaa 1301

<210> 60
 <211> 271
 <212> PRT
 <213> Salsola komarovii

<400> 60
 Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn Leu
 1 5 10 15
 Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln Glu
 20 25 30
 Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu Phe
 35 40 45
 Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu Thr
 50 55 60
 Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro Asp
 65 70 75 80
 Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val Leu
 85 90 95
 Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe Glu
 100 105 110
 Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile Pro
 115 120 125
 Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu Glu
 130 135 140
 Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg Ile
 145 150 155 160
 Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met Lys
 165 170 175
 Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser Asp
 180 185 190
 Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val Glu

195		200		205
Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn Val				
210		215		220
Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val Leu				
225		230		235
Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg Ile				
	245		250	255
Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu				
	260		265	270

<210> 61
 <211> 1032
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (1) .. (732)

<400> 61	
cca caa cga aga ccc gac ccg gtc ccg aac ctt cac ggt cag ctt ttt	48
Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe	
1 5 10 15	
caa cac cga aat cca cac cac cgt gac ctc cac ccc tgc cgt agc ccg	96
Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro	
20 25 30	
gca atg ggt cca ctc cct ccg cag act cat ctg cgc tgg tat tcc ctc	144
Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu	
35 40 45	
tcg cgc tac tcc ccc gtg atc ggc ctc ggc gtc caa tgg aag ccc tcc	192
Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser	
50 55 60	
tcc acc tca gct gcc act ctt caa ctc agc atc gac aaa aag tgc ctc	240
Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu	
65 70 75 80	
atc ttc caa ctc tcc cac tcc ccc gcc atc ccc gcc acc ctc cgc gac	288
Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp	
85 90 95	
ctc ctc ctc gac gat cgc gtc acc ttc ttt ggt gtc cac aac ggc cgt	336
Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg	
100 105 110	
gcc cgc gac ctc ctc caa ggg tcc cac cat gag ctc gac gtc aac aat	384
Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn	
115 120 125	

ctg gtt gat ctt gcc gag gag gaa aat ggt cat tac ttg aag tgg tcc 432
Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser
130 135 140

atg gaa gac atg gct gaa gat gtg ttg ggc ttt tgt ggg gta cac aaa 480
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys
145 150 155 160

ccc agg aag gtt atg tta agt ggt tgg gat cag tat tgc ttg tct aat 528
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn
165 170 175

gac cag gtt cag tat gct tgt gtt gat gct tac gtt tct ctt cgt ctt 576
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu
180 185 190

gct cga gct tat ggg tac cac cgt ctc gat cac gat gat gat tat gat 624
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp
195 200 205

gac cat gac gac gat gat aac gac cac acc gat gat gat tac gat gac 672
Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp
210 215 220

gtt tac gac cgc aat ata ggc tct gat gat gat ggt tat gat gcc gat 720
Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp
225 230 235 240

gat gat cga cga tgatcaattt ggactagact tcgttattgg aagggtccga 772
Asp Asp Arg Arg

tcatcatgcc agtctaatta caaagagaca agaaataaaa atgatgatca aaaaaagaag 832

tcaatccata tacgtaattt tcattgcaat atcaattttg aggtgtttta ttattggcct 892

gtaataatag ttttatttaa taatagcact atagatctca tcctaaccctt tacttattgg 952

gcttatgcgc tgtatgtcca ataaccaagt ttaatttatt tcatgatctg atgattactg 1012

caaaaaaaaa aaaaaaaaaa 1032

<210> 62

<211> 244

<212> PRT

<213> Salsola komarovii

<400> 62

Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
1 5 10 15

Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro
20 25 30

Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu
35 40 45

Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser
 50 55 60
 Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu
 65 70 75 80
 Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp
 85 90 95
 Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg
 100 105 110
 Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn
 115 120 125
 Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser
 130 135 140
 Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys
 145 150 155 160
 Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn
 165 170 175
 Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu
 180 185 190
 Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp
 195 200 205
 Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp
 210 215 220
 Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp
 225 230 235 240
 Asp Asp Arg Arg

<210> 63
 <211> 1029
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (3) .. (824)

<400> 63
 ca cat atc agc cac atc cac tta att ccc cac agt ctt agt ctc tta 47
 His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu
 1 5 10 15
 gac acc cat ctt agt ctt aag cct ctc atg gcc acc gcg gta ttc tca 95

Asp	Thr	His	Leu	Ser	Leu	Lys	Pro	Leu	Met	Ala	Thr	Ala	Val	Phe	Ser	
				20					25					30		
cct	tct	gcc	ctt	cta	tcc	acc	tcc	aca	tcc	acc	tca	aca	acc	cct	ctt	143
Pro	Ser	Ala	Leu	Leu	Ser	Thr	Ser	Thr	Ser	Thr	Ser	Thr		Pro	Leu	
			35					40					45			
aaa	gct	ccc	ccc	ttg	gcc	tta	acc	aag	acc	cac	gta	acg	atc	cca	tca	191
Lys	Ala	Pro	Pro	Leu	Ala	Leu	Thr	Lys	Thr	His	Val	Thr	Ile	Pro	Ser	
		50					55					60				
tca	tca	aag	cca	ccc	cta	acc	aat	tta	act	acc	agt	tta	act	gct	gtc	239
Ser	Ser	Lys	Pro	Pro	Leu	Thr	Asn	Leu	Thr	Thr	Ser	Leu	Thr	Ala	Val	
	65					70					75					
gcc	aca	gct	gct	gcc	ata	atc	ctg	tcc	aca	acc	cct	cca	tcg	ttt	gct	287
Ala	Thr	Ala	Ala	Ala	Ile	Ile	Leu	Ser	Thr	Thr	Pro	Pro	Ser	Phe	Ala	
	80				85					90					95	
gat	gat	ttg	cag	aca	aat	gca	tac	aac	att	tac	tac	ggc	act	gct	gca	335
Asp	Asp	Leu	Gln	Thr	Asn	Ala	Tyr	Asn	Ile	Tyr	Tyr	Gly	Thr	Ala	Ala	
			100					105						110		
agt	gca	gcc	aat	tat	gga	ggc	tac	ggg	ggc	aat	tcg	aac	aag	aaa	gat	383
Ser	Ala	Ala	Asn	Tyr	Gly	Gly	Tyr	Gly	Gly	Asn	Ser	Asn	Lys	Lys	Asp	
			115					120					125			
tca	gct	gag	tac	ata	tat	gac	gtc	cct	gca	ggg	tgg	aaa	gag	aga	cta	431
Ser	Ala	Glu	Tyr	Ile	Tyr	Asp	Val	Pro	Ala	Gly	Trp	Lys	Glu	Arg	Leu	
		130					135					140				
gta	tca	aaa	gtt	gag	aag	ggg	acc	aat	gga	aca	gat	agt	gag	ttc	ttc	479
Val	Ser	Lys	Val	Glu	Lys	Gly	Thr	Asn	Gly	Thr	Asp	Ser	Glu	Phe	Phe	
	145					150					155					
aac	ccc	aag	aag	aag	aca	gag	cga	gag	tac	ctt	acc	tac	ctt	gct	ggg	527
Asn	Pro	Lys	Lys	Lys	Thr	Glu	Arg	Glu	Tyr	Leu	Thr	Tyr	Leu	Ala	Gly	
	160				165					170					175	
att	agg	caa	cta	ggg	ccc	aaa	gaa	gtg	atc	ctc	aac	aac	tta	gca	ctc	575
Ile	Arg	Gln	Leu	Gly	Pro	Lys	Glu	Val	Ile	Leu	Asn	Asn	Leu	Ala	Leu	
			180					185						190		
tca	gat	gtg	aac	ctg	caa	gat	caa	att	tcc	agt	gca	gac	tct	gtg	aca	623
Ser	Asp	Val	Asn	Leu	Gln	Asp	Gln	Ile	Ser	Ser	Ala	Asp	Ser	Val	Thr	
			195					200					205			
tca	gaa	gag	agg	aaa	gat	gac	aag	gga	cag	gtt	tac	tat	gat	tat	gag	671
Ser	Glu	Glu	Arg	Lys	Asp	Asp	Lys	Gly	Gln	Val	Tyr	Tyr	Asp	Tyr	Glu	
		210					215					220				
att	gct	gga	gct	ggg	tca	cac	agt	ttg	ata	tcg	gta	aca	tgt	gcc	agg	719
Ile	Ala	Gly	Ala	Gly	Ser	His	Ser	Leu	Ile	Ser	Val	Thr	Cys	Ala	Arg	
	225					230					235					
aac	aag	cta	tat	gcg	cat	ttt	gtt	agc	gca	cca	aca	ccc	gaa	tgg	aat	767
Asn	Lys	Leu	Tyr	Ala	His	Phe	Val	Ser	Ala	Pro	Thr	Pro	Glu	Trp	Asn	

240 245 250 255
 cgg gat caa gat atg ctg agg cac atc cac aac tca ttt aca aca gtc 815
 Arg Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val
 260 265 270
 ggg tca ttc tagaaagtgt atatgataat catttataga gatgtcagag 864
 Gly Ser Phe
 aggcatatcat ttgaatgtac ttctgatgag ctggacttct tgatctatgt aacattgtaa 924
 cgaaaattct ttctgggtta tcagaaacct agtgagtgtc tgaaacttgc aatgagaaac 984
 tcttcaataa acaatgactt gtatcaaaaa aaaaaaaaaa aaaaa 1029

<210> 64
 <211> 274
 <212> PRT
 <213> Mesembryanthemum crystallinum

<400> 64
 His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu Asp
 1 5 10 15
 Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser Pro
 20 25 30
 Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Thr Pro Leu Lys
 35 40 45
 Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser Ser
 50 55 60
 Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val Ala
 65 70 75 80
 Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala Asp
 85 90 95
 Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala Ser
 100 105 110
 Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp Ser
 115 120 125
 Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu Val
 130 135 140
 Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe Asn
 145 150 155 160
 Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly Ile
 165 170 175
 Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu Ser
 180 185 190

Asp	Val	Asn	Leu	Gln	Asp	Gln	Ile	Ser	Ser	Ala	Asp	Ser	Val	Thr	Ser
		195					200					205			
Glu	Glu	Arg	Lys	Asp	Asp	Lys	Gly	Gln	Val	Tyr	Tyr	Asp	Tyr	Glu	Ile
		210				215					220				
Ala	Gly	Ala	Gly	Ser	His	Ser	Leu	Ile	Ser	Val	Thr	Cys	Ala	Arg	Asn
225					230					235					240
Lys	Leu	Tyr	Ala	His	Phe	Val	Ser	Ala	Pro	Thr	Pro	Glu	Trp	Asn	Arg
				245					250					255	
Asp	Gln	Asp	Met	Leu	Arg	His	Ile	His	Asn	Ser	Phe	Thr	Thr	Val	Gly
			260					265					270		

Ser Phe

<210> 65
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Primer

<400> 65
 gctctgagaa ccgtctagac ttagatgaag gtg 33

<210> 66
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Primer

<400> 66
 tctctcggtc atctcgagct attacagctc 30

,P
 ,U,Q□^,X,P